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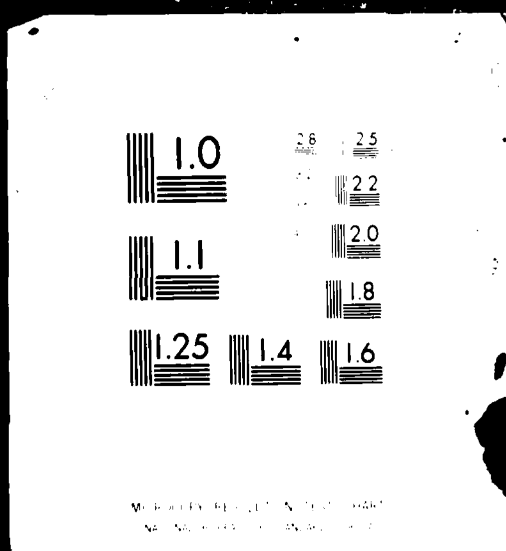

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A stereophotometric data set, describing the body surface of a subject, was segmented into nineteen groups of stereophotometric data, the data in each group describing the surface of a body segment. The process was repeated for a total of 59 such data sets. The data resulting from each of these segmentation processes were then analyzed for inertial properties and location and orientation of both anatomical and principal axis systems. The accumulated body volume as a function of vertical distance from the floor was also

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Block 20 - Abstract (Continued)

tabulated for all the data sets.

SUMMARY

This report outlines work done by the University of Dayton Research Institute (UDRI) under Contract No. F33615-78-C-0504 to analyze s ereophotometric data sets. These data sets were prepared by the Texas Institute for Rehabilitation and Research, and consist of stereophotometric data describing the body surfaces of 46 different female subjects.

The first step in the analysis of this data was to sort data points for each subject into 19 groups. Each of these groups then consisted of data points describing the surface of one of the body segments illustrated in Figure 3 of this report.

The data sets resulting from this sorting or segmentation were then used as input to program IMPED, a FORTRAN coded computer program written jointly by the UDRI and the Mathematics and Analysis Branch of the Air Force Aerospace Medical Research Laboratory. A sample listing of all analyses performed on the segmented data by program IMPED is given in Appendix I. The portions of IMPED written by the UDRI include subroutines to compute inertial properties for specified combinations of body segments, location and direction cosines of the segment principal axis systems from the directions associated with the principal moment vectors, and tabulation of percent height versus percent volume from the floor to specified heights for each subject's data set.

The results of these analyses provide information describing inertial and geometric properties for each of the 46 subjects.

PREFACE

This is the final report for work performed by the University of Dayton Research Institute (UDRI) under Contract No. F33615-78-C-0504. Sponsor for this contract was the Mathematics and Analysis Branch of the Air Force Aerospace Medical Research Laboratory (AFAMRL/BBM). Mr. L. Douglas Baughman served as principal investigator for the UDRI. The UDRI student research assistant, Mr. Jeffrey Beers, also assisted with work performed under this contract, and, in particular, is responsible for the work described in Paragraph 3.4 of this report. Mr. Ints Kaleps (Chief, AFAMRL/BBM) served as technical monitor for this contract. The author would also like to acknowledge the contributions of two UDRI employees: Mr. Dart G. Peterson who performed technical editing of this report, and Ms. Charlene Thompson who did the typing necessary for this report.

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GLOSSARY OF TERMS

Acromiale (right and left): The most lateral point on the lateral margin of the acromial process of each scapula.

Anatomical Axis System: A right-handed, three dimensional axis system, defined by anthropometric landmarks. One such axis system is defined for each body segment.

Anterior Superior Iliac Spine (right and left): The inferior point of each anterior superior iliac spine.

Anthropometry: Study of the physical dimensions of the human body.

Articulated Total Body Model: Computer/mathematical model used to simulate the motion of the human body in a dynamic environment.

Bustpoint (right and left): The maximum anterior protrusion of a bra cup.

Cervicale: The superior tip of the spine of the seventh cervical vertebra. (The protrusion of the spinal column at the base of the neck.)

Clavicale (right and left): The point on the most imminent prominence of the superior aspect of the medial end of each clavical.

Cross Section: The collection of data points describing the contour around a subject's body at some horizontal level.

Crotch Sensor: The subject stands, feet slightly apart and a spring loaded pole, with a cross bar forming a T at the top, is placed in the apex of the crotch. The anterior point on the cross bar is located photometrically.

Dactylion (right and left): The tip of digit III of each hand.

Direction Cosine Matrix: A three by three matrix used to relate the orientation of one axis system to another. If $D=(d_{ij})$ is the cosine matrix of axis system A with respect to axis system B, then d_{ij} is the cosine of the angle between i^{th} axis (1=X, 2=Y, 3=Z) of the A system and the j^{th} axis of the B system (assuming the axis systems have been translated so that their origins coincide).

Femoral Epicondyle, Lateral (right and left): The lateral point on the lateral epicondyle of each femur.

Femoral Epicondyle, Medial (right and left): The medial point on the medial epicondyle of each femur.

Fibulare (right and left): The proximal tip of each fibula.

Fiducial: A marker attached to a subject's body in order to locate a landmark during the digitization process.

FLAPS: The second program in the set of segmentation programs. It is used to separate out data points describing the shoulder and hip flaps.

Global Axis System: A right handed axis system. The X-Y plane of this axis system corresponds to the standing surface of the subject, and the Y-axis is defined by the projection of the line segment connecting the left and right anterior superior iliac spines onto the X-Y plane. The origin is the mid-point of this line segment. Positive Y is to the subject's left and positive Z upward.

Gluteal Fold (right and left): The lowest point on each gluteal fold.

Gonion (right and left): The lateral and inferior point on the back of the mandible at the intersection of the vertical and horizontal portions of each side of the jaw.

Head Circumference: A point in the midsagittal line of the forehead just above the brow ridges.

Humeral Epicondyle, Lateral (right and left): The lateral point on the lateral epicondyle of each humerus with the arms in the anatomical position.

Humeral Epicondyle, Medial (right and left): The medial point on the medial epicondyle of each humerus with the arm in the anatomical position.

Iliocristale Points (right and left): The highest point on the crest of each ilia in the midaxillary line.

IMPED: Computer program written jointly by the AFAMRL/BBM and the UDRI to perform analyses of the stereophotometric data.

Inertial Properties: Properties computed by Program IMPED for each body segment including mass, center of gravity, and magnitude and direction of principal moments of inertia.

Infraorbitale (right and left): The lowest point on the inferior margin of each orbit.

Landmark: Easily identified locations on the human body.

Malleoli, Lateral (right and left): The most lateral point on each lateral malleolus.

Metacarpale II (right and left): The most laterally prominent point on the lateral surface of the head of the second metacarpal, with the hand in the anatomical position.

Metacarpale III (right and left): The distal point in the midline on the head of the third metacarpal with the hand rotated 180° from the anatomical position.

Metacarpale V (right and left): In the anatomical position, the most medially prominent point on the medial surface of the head of the fifth metacarpal.

Metatarsal I (right and left): The medial point on the head of each metatarsus I.

Metatarsal V (right and left): The lateral point on the head of each metatarsus V.

Mid-thyroid Cartilage: The anterior point in the midsagittal plane of the thyroid cartilage.

Nuchale: The lowest point in the midsagittal plane of the occiput that can be palpated among the muscles in the posterior-superior part of the neck. This point will usually be obscured by hair.

Olecranon (right and left): The superior point on the olecranon process of the ulna with each arm in the anatomical position.

POLISH: The third of the three segmentation routines. This computer program produces a header for the stereophotometric data, combines the shoulder flaps with their respective upper arms, and creates a cross-section between the thorax and abdomen, and another one between the abdomen and pelvis.

Posterior Calcaneous Point (right and left): The posterior point on each heel.

Posterior Superior Iliac Midspine: The point on the midspine made at the level of the posterior-superior iliac spines. (A dimple often indicates the site of this iliac spine.)

Principal Axis System: A right-handed axis system, one of which is defined for each body segment. The orientation and location of these axis systems depends upon the mass distribution of its associated segment.

Radial Styloid (right and left): The point at the distal tip of the radius.

Radiale (right and left): The highest palpable point on the head of each radius with the arm in the anatomical position.

Scye Points (right and left): These are a series of marks drawn at the axillary folds formed by the juncture of the arms and trunk. Subject stands and initially abducts slightly her right arm; a straight edge is placed horizontally under the armpit so that the top of the straight edge touches, without compressing the tissue, the inferior point of the axillary fold. The subject then relaxes the arm and short horizontal lines are drawn at the level of the top of the straight edge on the anterior and posterior surfaces of the arms and torso. The process is repeated on the left side of the body. The intersections of the horizontal marks and the vertical lines following the axillary folds in the direction of the acromion are the scye point landmarks.

Segmentation: Separation of stereophotometric data points into groups, each group then describing the surface of one body segment.

Segmenting Plane: Planes used to define the separation between body segments.

Sellion: The point in the midsagittal plane of the deepest depression of the nasal root.

SGMNTS: The first of the three segmentation routines. This computer program groups data points so that a total of 17 body segments are defined at its completion.

Sphyrion (right and left): The distal end of each tibia.

Stereophotometrics: A process used to obtain data points describing the body surface of a subject. Simultaneous photographs are taken of the subject from different angles. These photographs are then computer digitized yielding the location of data points on the surface of the subject's body.

Suprasternale: The lowest point of the jugular notch on the superior margin of the sternum.

Symphysion: The anterior point in the midsagittal plane on the notch of the superior border of the pubic symphysis.

Tenth Rib (right, left, and midspine): A series of marks in the midspine, in the midaxillary line, made at the level of the lowest point on the inferior margin of the lowest of the two tenth ribs.

Tibiale (right and left): The superior point on the medial margin of the head of each tibia.

Toe II (right and left): The tip of digit II of each foot.

Tragion (right and left): The deepest point of the notch just above the tragus of each ear.

Trochanterion (right and left): The proximal point of the greater trochanter of each femur.

Ulnar Styloid (right and left): The distal point of each ulna.

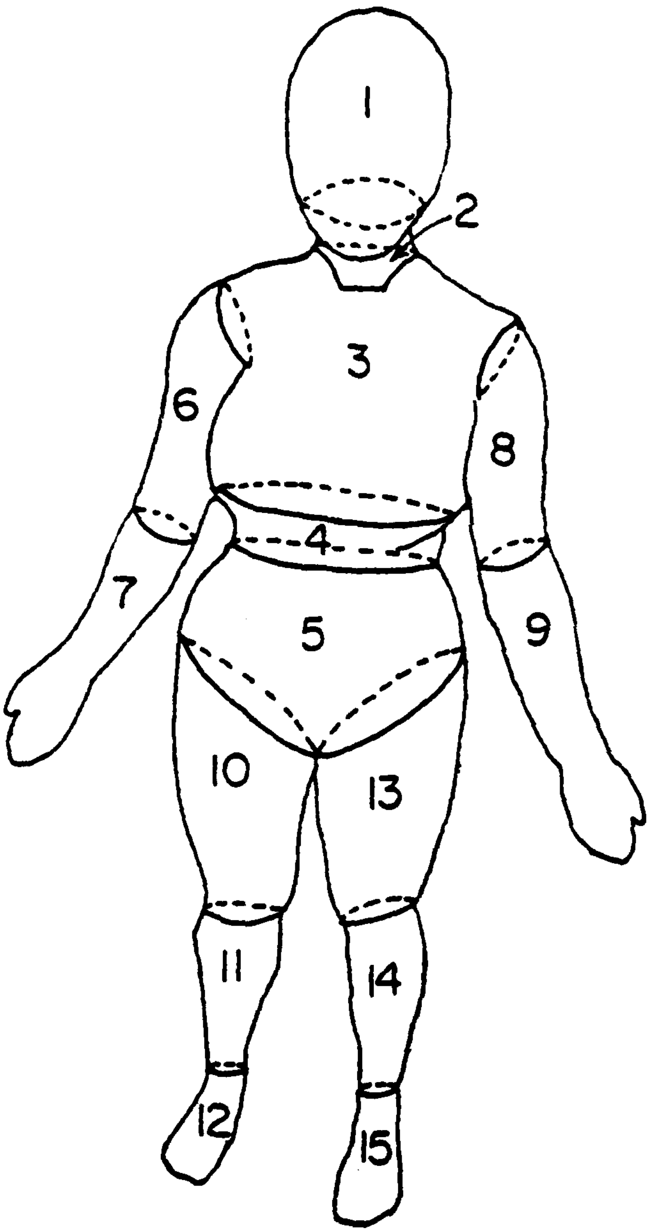
LIST OF ABBREVIATIONS, ACRONYMS, AND SYMBOLS

AFAMRL/BBM	- Mathematics and Analysis Branch of the Air Force Aerospace Medical Research Laboratory
ASIS	- Anterior Superior Iliac Spine
ATB Model	- Articulated Total Body Model
TIRR	- Texas Institute for Rehabilitation and Research
UDRI	- University of Dayton Research Institute
•	- dot or scalar product of two vectors
x	- cross product of two vectors

SECTION 1
INTRODUCTION

The development of mathematical/computer models capable of predicting the motion of the human body in a dynamic environment has created a need for extensive data describing human geometry and inertial properties. These models have been used to predict body motion during events such as automobile crashes and aircraft cockpit ejections, and are capable of pointing out potentially hazardous designs of these two environments. One such model is the Articulated Total Body (ATB) Model (Fleck and Butler, 1975) developed under sponsorship of the Mathematics and Analysis Branch of the Air Force Aerospace Medical Research Laboratory (AFAMRL/BBM). The ATB Model models the human body as a series of connected rigid bodies, referred to as body segments. The ATB Model is flexible as to how many segments are used to define the human body. There is, however, a standard configuration, consisting of 15 segments, which is illustrated in Figure 1.

Body description data required by the ATB Model for each body segment include: center of gravity of the segment, segment mass, principal moments of inertia, and the directions associated with these moments. In the past, cadaver studies, such as those performed by Chandler, et al. (1975) and Walker, et al. (1973), have been used as a source for the body description data. An alternative approach has been to construct geometric models approximating body segments. These models are such that the needed data items are known functions of the model's dimensions, and these dimensions may be computed from standard anthropometric measurements. This is the method used by Reynolds (1976). This approach was also undertaken during the early months of this contract (F33615-78-C-0504), using more elaborate geometric models than others had previously in order to better approximate body segments. The details of this study may be found in Leet (1978).



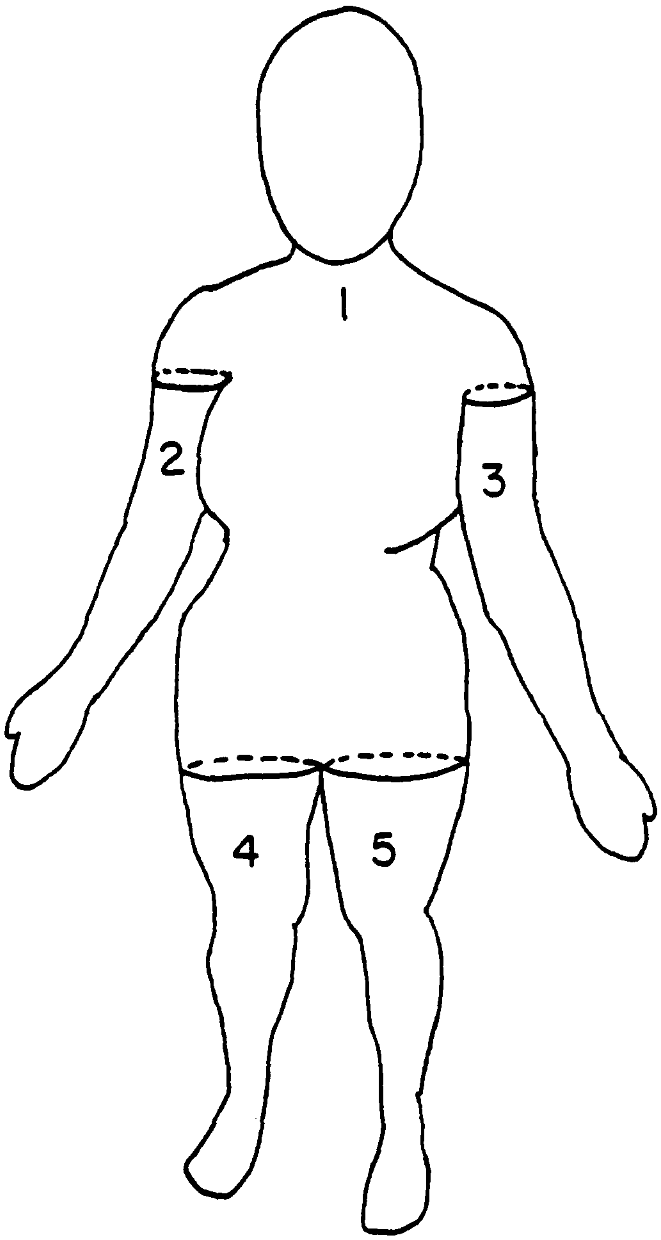
1. Head
2. Neck
3. Thorax
4. Abdomen
5. Pelvis
6. Right Upper Arm
7. Right Lower Arm
8. Left Upper Arm
9. Left Lower Arm
10. Right Thigh
11. Right Calf
12. Right Foot
13. Left Thigh
14. Left Calf
15. Left Foot

Figure 1. Fifteen Segment Configuration Commonly Used With Articulated Total Body (ATB) Model.

A technique, referred to as stereophotometry, has been developed (Herron et al., 1974) to obtain three dimensional body description data. This technique involves the taking of simultaneous pairs of photographs of a subject from the front and rear by spatially separated cameras. Data from these stereophotographs are then computer digitized in a systematic fashion which provides coordinates of points on the surface of the subject's body. The digitization process is performed in such a way that the data points it yields are arranged in horizontal body cross sections. Assuming homogeneity of the body, numerical integration may then be applied to this data as a means of obtaining inertial data for that subject. The Texas Institute for Rehabilitation and Research (TIRR) recently applied the stereophotometric technique to a group of 46 female subjects producing a body surface description data set for each subject. For some of the subjects the method was applied more than once, as a check on the reproducibility of all results, giving a total of 59 data sets. These were handled as data sets describing 59 unique subjects throughout the work described in this report.

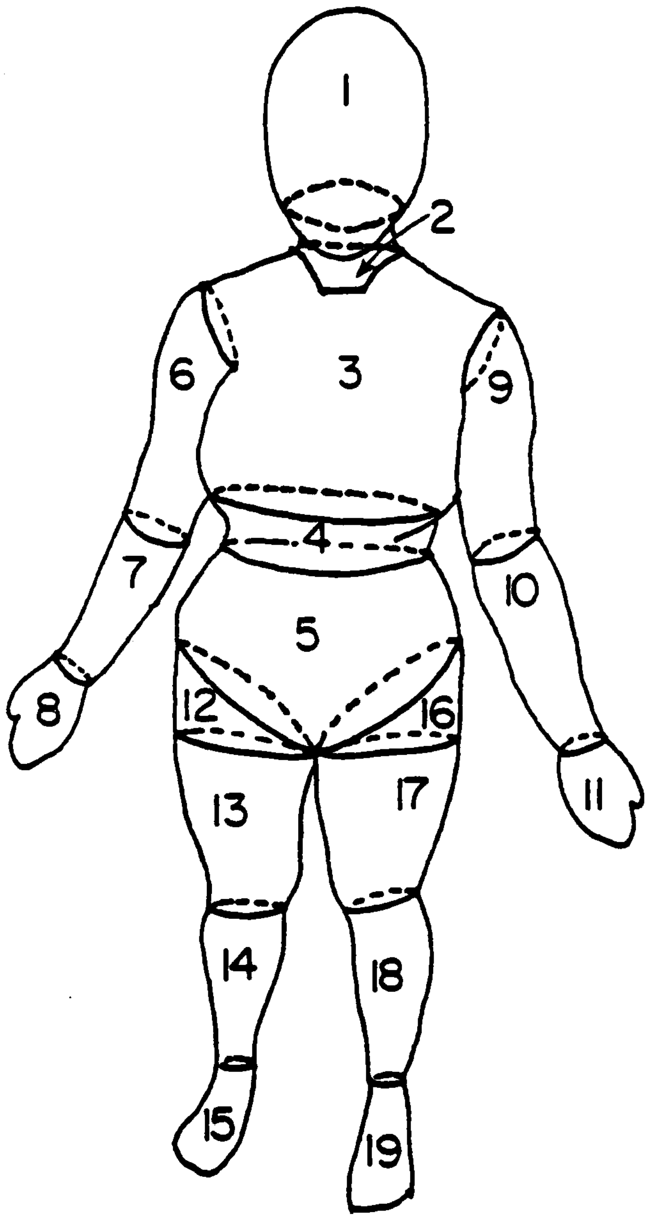
Each data set prepared by Texas Institute for Rehabilitation and Research (TIRR) has data points sorted into five groups: one group of data points describes the surface of the head and trunk regions of the body, two describe the arms, and two describe the legs. These five sections of the body will be referred to as TIRR segments and are illustrated in Figure 2. In order for the results of analyzing these data to be usable in terms of the ATB Model, the results must be configured in terms of, at least, the 15 body segments shown in Figure 1. Thus, prior to analyzing the data, the data points must be regrouped according to a larger set of body segments. The procedures used to regroup the data, referred to as segmentation routines, are outlined in Section 2.

To be consistent with the work that has been performed by McConville et al. (1980) the data points for each subject were regrouped into 19 groups. Each of these 19 groups contains data points describing one of the body segments shown in Figure 3. The difference between these 19 segments and the 15 defined for the ATB Model



1. Head-Trunk
2. Right Arm
3. Left Arm
4. Right Leg
5. Left Leg

Figure 2. Five Segment Configuration of Texas Institute for Research and Rehabilitation (TIRR) Data.



1. Head
2. Neck
3. Thorax
4. Abdomen
5. Pelvis
6. Right Upper Arm
7. Right Forearm
8. Right Hand
9. Left Upper Arm
10. Left Forearm
11. Left Hand
12. Right Hip Flap
13. Right Thigh Minus Flap
14. Right Calf
15. Right Foot
16. Left Hip Flap
17. Left Thigh Minus Flap
18. Left Calf
19. Left Foot

Figure 3. Nineteen Segment Data Configuration as Produced by Segmentation Routines.

(see Figure 1) is that each ATB Model lower arm has been separated into a forearm and hand, and each ATB Model thigh has been separated into a hip flap and thigh minus flap. Inertial properties calculated for the 19 segment model, are applicable to the 15 segment model, since it is a simple process to combine the inertial properties of two or more segments into one segment.

The segmentation routines, after sorting data points by segment, distinguish between segment representing groups in the data in the same manner as did TIRR in the preparation of its data set. All cross sections containing data points belonging to the first segment are listed first, followed by those with data points belonging to the second segment, etc. The numbers associated with the TIRR segments and the 19 segments after segmentation are the same as in Figures 2 and 3, respectively. Cross sections belonging to the same segment are listed in order of decreasing Z (vertical axis) coordinate. The data for a cross section are presented in a format (see Appendix G) that gives first the cross section number, number of data points in the cross section, and the Z coordinate common to all of the points in the cross section. This is followed by a list of the X,Y coordinates of the data points in that cross section. Cross sections are numbered in the order that they are listed within a segment representing group. Thus the cross section in each segment with the largest Z coordinate has a cross section number of one, and each cross section numbered one signals the beginning of the next segment representing group.

After the segmentation of the stereophotometric data numerous analyses were performed on the segmented data by a FORTRAN coded computer program, IMPED. Appendix I is a complete listing of the results of these analyses for one subject's data set. The writing of IMPED was performed jointly by members of the AFAMRL/BBM and the UDRI. Portions of IMPED which calculate principal moments of inertia and their associated directions, volume, and center of gravity for each of the 19 segments were written by members of the AFAMRL/BBM. Portions of IMPED written by the UDRI determine the principal moments of inertia for certain specified combinations of the 19 segments

(including those combination segments used in the ATB Model) and tabulate partial body volume as a function of distance from the standing surface. Additionally, portions of IMPED written by the UDRI determine the location and orientation of segment principal and anatomical axis systems, and the location of certain landmark and other points relative to these two axis systems. These analyses carried out by portions of IMPED written by the UDRI are discussed in more detail in Section 3.

SECTION 2
SEGMENTATION ROUTINES

The division between two adjacent body segments is defined by one or more planes (see Table 1), referred to as segmenting planes. For each segmenting plane a normal vector and a point on the plane are specified. As an initial approach, consider the problem of separating the data points between two segments.

By taking a vector from a point on the segmenting plane (the point used in defining the segmenting plane is used in practice) to any point in question, and dotting this vector with the specified normal to the segmenting plane, the segment the point in question belongs to is determined. If the dot product is positive the point lies in one segment, if negative it lies in the other segment. Some of the segments are separated by more than one segmenting plane. Points are separated between such segments by specified combinations of positive and negative dot products (see Table 2).

To the extent possible, the separation of data points into groups corresponding to the 19 segments shown in Figure 3 is reduced to the problem of separating data points between two segments, as has just been described. The actual work of separating data points is performed by three computer programs: program SGMNTS, program FLAPS, and program POLISH. SGMNTS is run first, segmenting the data prepared by TIRR into the 17 segments shown in Figure 4a. These 17 segments leave the right and left shoulder flaps part of the thorax and the right and left hip flaps part of the pelvis. FLAPS is then run twice. On its first run it separates out data points belonging to the left shoulder flap and left hip flap (see Figure 4b), and on its second run it separates out the right shoulder and hip flaps (see Figure 4c). Lastly POLISH is run. It combines the shoulder flap data points with their respective upper arm segments, adds a cross section between the thorax and abdomen and one between the abdomen and pelvis, and prepares a header for the data set. The data produced by POLISH is in its final form and ready for analysis by program IMPED. A listing of these three programs is given in Appendix F.

TABLE 1

DEFINITION OF SEGMENTING PLANES

SEGMENTS SEPARATED	NORMAL VECTOR TO PLANE	LANDMARK POINT LYING IN SEGMENTING PLANE
Head-Neck	$(L_{40}-L_{39}) \times (L_1-L_{39})^*$	L_{39}
Neck-Thorax #1	$(0, 0, 1)^{**}$	L_2
#2	$(0, 1, 1)$	L_{43}
#3	$(0, 0, 1)$	L_{43}
Thorax-Abdomen	$(0, 0, 1)$	L_7
Abdomen-Pelvis	$(0, 0, 1)$	L_{32}
Right Upper Arm - Forearm	$(L_{10}-L_{12}) \times (L_{14}-L_{12})$	L_{14}
Right Forearm - Hand	$(0, L_{16_Y}-L_{20_Y}, L_{16_Z}-L_{20_Z})^{***}$	L_{22}
Left Upper Arm - Forearm	$(L_9-L_{13}) \times (L_{11}-L_{13})$	L_{13}
Left Forearm - Hand	$(0, L_{15_Y}-L_{19_Y}, L_{15_Z}-L_{19_Z})$	L_{21}
Right Thigh - Calf	$(0, 0, 1)$	L_{59}
Right Calf - Foot	$(0, 0, 1)$	L_{69}
Left Thigh - Calf	$(0, 0, 1)$	L_{58}
Left Calf - Foot	$(0, 0, 1)$	L_{68}
Right Shoulder Flap-Thorax #1	$(L_4-L_6) \times (0, 1, 0)$	L_4
#2	$(0, 0, -1)$	L_{77}
Left Shoulder Flap-Thorax #1	$(L_5-L_3) \times (0, 1, 0)$	L_3
#2	$(0, 0, -1)$	L_{78}
Right Hip Flap-Pelvis	$\left(\frac{L_{34}+L_{37}}{2} - L_{35}\right) \times (0, 1, 0)$	L_{35}
Left Hip Flap-Pelvis #1	$\left(L_{35} - \frac{L_{33}+L_{36}}{2}\right) \times (0, 1, 0)$	L_{35}
#2	$(1, 0, 0)$	L_{35}

*L_i refers to the vector to the i^{th} landmark. The names of these landmarks may be found in Table 1 of Appendix I, for i=1, ..., 76. For i=77 or i=78, these are the two landmarks created by Program SGWTS and described in the beginning of Section 2.

**These vectors correspond to an axis system in which the X axis points to the subject's right, the Y axis points to the forward direction of the subject, and the Z axis points upward.

***L_{i_X}, L_{i_Y}, L_{i_Z} refer to the X, Y, or Z coordinate of landmark i, respectively.

TABLE 2

LOGIC APPLIED FOR SEGMENTS SEPARATED BY MORE THAN ONE SEGMENTING PLANE

SEGMENTS SEPARATED	LOGIC APPLIED IF	LOGIC APPLIED THEN
Neck-Thorax	$dot_1^* > 0$ or ($dot_2 > 0$ and $dot_3 > 0$)	Point belongs in neck.
	Otherwise	Point belongs in thorax.
Right Shoulder Flap-Thorax	$dot_1 > 0$ or $dot_2 > 0$	Point belongs in thorax.
	Otherwise	Point belongs in flap.
Left Shoulder Flap-Thorax	$dot_1 > 0$ or $dot_2 > 0$	Point belongs in thorax.
	Otherwise	Point belongs in flap.
Left Hip Flap - Pelvis	$dot_1 > 0$ or $dot_2 > 0$	Point belongs in pelvis.
	Otherwise	Point belongs in flap.

* dot_i refers to the dot product computed for the i^{th} segmenting plane, separating the two segments (see Table 1).

2.1 PROGRAM SGMNTS

Program SGMNTS performs the initial grouping of data points into body segments. It receives the data prepared by TIRR, which is separated into five segments, and further separates it into a total of 17 segments. Each data point output by SGMNTS will be grouped into one of the body segments shown in Figure 4a.

Definition of segmenting planes, necessary to perform this separation of data, is accomplished by use of anthropometric landmarks (see Table 1). Prior to photographing a subject, TIRR placed a fiducial at each of the 76 landmarks. In most cases two locations were then recorded for each landmark by the digitization process performed on the photographs. The tip of the fiducial, furthest from the surface of the skin, is one of the two locations recorded, and is referred to as the distal point. The other point recorded may be anywhere along the fiducial, and is referred to as the proximal point. The fiducials used are three-quarters of an inch long. Thus the actual landmark, on the surface of the skin, lies on the line defined by the proximal and distal points, three-quarters of an inch from the distal point in the direction of the proximal point. In some cases TIRR was able to directly record the actual location of a landmark. When this was possible, it was indicated in the data by assigning all three coordinates of the proximal point a value of zero. The distal point then takes on the location of the landmark. Program SGMNTS computes the actual coordinates for all 76 landmarks, and writes these coordinates out in order that they may be used directly by subsequent programs, as well as making use of these landmark locations itself.

Additionally SGMNTS determines two Z coordinates. One of these is computed to be the average of the Z coordinate of the first cross section of the left TIRR arm segment and the smallest Z coordinate of any cross section in the TIRR head-trunk segment that is greater (strictly) than this first Z coordinate of the left arm. This process is repeated using the right arm. The resulting two Z coordinates are written out by SGMNTS as the Z coordinate of a seventy-seventh and seventy-eighth landmark, each of these having X and Y coordinates of

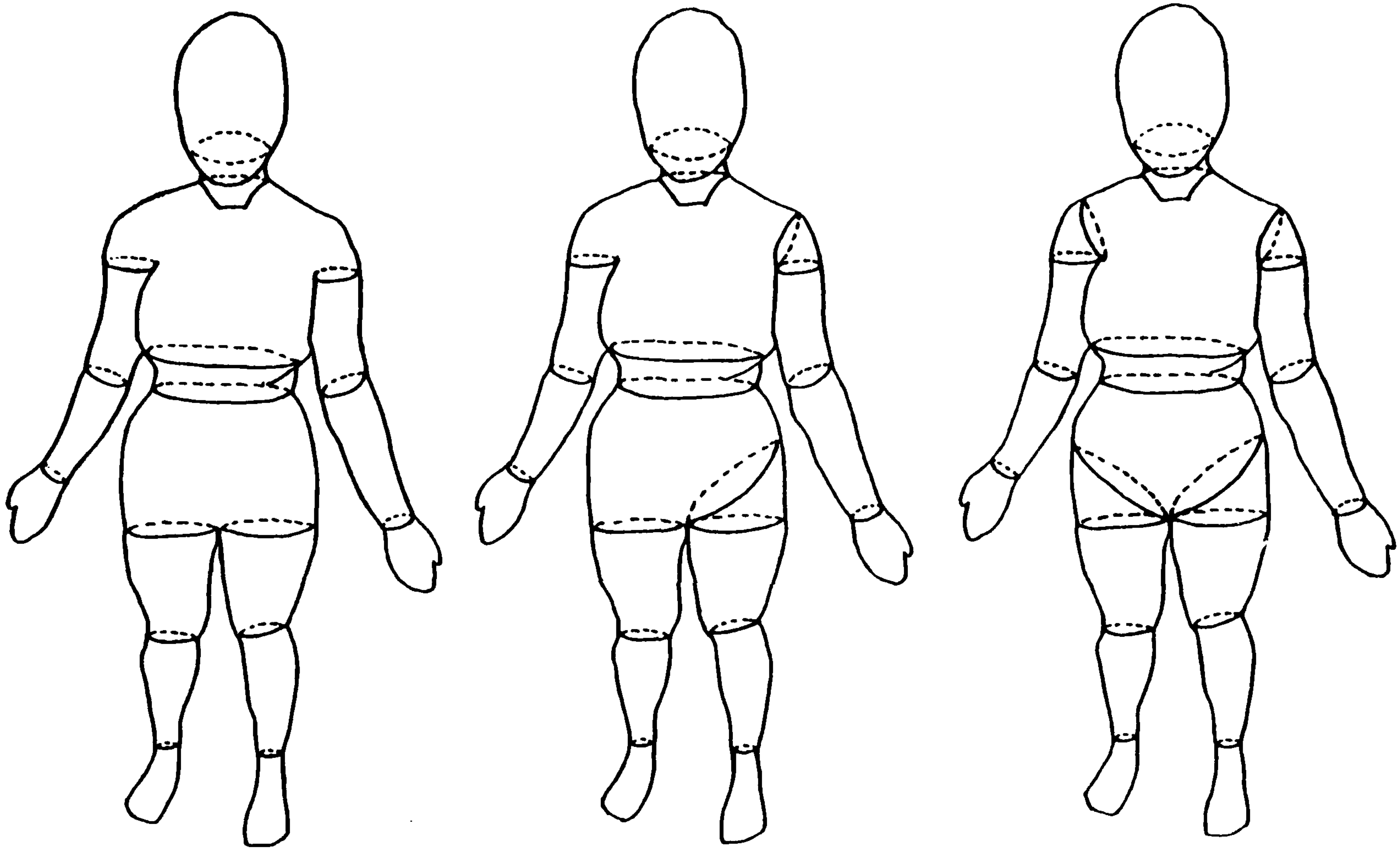


Figure 4. Segments Defined at Intermediate Steps of Segmentation.

(a) Output from Program SGMNTS; Input to Run No. 1 of Program FLAPS.
(b) Output from Run No. 1 of Program FLAPS; Input to Run No. 2 of Program FLAPS.
(c) Output from Run No. 2 of Program FLAPS; Input to Program POLISH.

zero (simply as a space filler). These two Z coordinates are then used by program FLAPS to define two of the segmenting planes it uses. Prior to writing out the final set of data by program POLISH, these two landmarks are removed.

Two observations were made on the arrangement of the 17 segments that program SGMNTS divides data points into (see Figure 4a). These observations have been used to simplify the algorithm used by SGMNTS.

1. The data points in any one horizontal cross section of one of the TIRR segments can belong to at most two of the 17 segments.

2. When comparing two segments, which are part of the same TIRR segment, it is always possible to speak of one as being above the other. That is, if A and B are two such segments, and the topmost cross section of A is above the topmost cross section of B, then the bottom-most cross section of A will be above the bottom-most section of B; A cannot be both above and below B.

Program SGMNTS deals with one TIRR segment at a time, working within each one from top to bottom.

Consider, for example, the TIRR head-trunk segment. As program SGMNTS begins examining this TIRR segment it compares all the points within the topmost cross section with the segmenting plane separating the head and neck. Comparison need only be made to this one segmenting plane since, by Observation 1, all points within this cross section must belong to either the head or the neck. The individual data points in this cross section are compared to the segmenting plane by means of a dot product as previously described (refer also to the beginning of Appendix A). All segmenting planes used by program SGMNTS are oriented so that their normal vectors point to the segment above the plane, and thus, for this first cross section of the TIRR head-trunk segment, all of these dot products should be positive. This, of course, indicates that all data points in the first cross section belong to the head segment. Since all of these data points do belong to the head segment, data for this cross section are simply written out as read in.

This process is repeated for each successive cross section, moving downward through the TIRR head-trunk segment. After some number of cross sections containing only data points belonging to the head have been processed, an area of overlap between the head and neck will be encountered. This will be signaled by a cross section containing some data points that produce positive dot products, and others that will produce negative dot products. The negative dot products indicate that their associated data points do not belong to the head, but rather to the neck.

Program SGMNTS adds two data points to cross sections of this type. These points are added along the intersection between the horizontal plane of the cross section and the segmenting plane. The details of the computations used to locate these two points are listed in Appendix A. With this accomplished, the coordinates of all data points with negative dot products are stored by program SGMNTS, along with the two added points. The data set for this cross section is then reformed to include only those data points with associated positive dot products. The two added data points are included here also, since they belong to both the head and the neck. Data for this cross section are then written out with the count for the total number of data points being the number of data points with positive dot products, plus two.

This type of processing is repeated for each cross section containing some data points yielding positive dot products and others yielding negative dot products. After some number of these cross sections are processed, one cross section will be encountered in which the dot product for all data points is negative. This indicates that the segment immediately above the segmenting plane (in the case of this example, the head segment) has been completely processed. Note that by Observation 2, it is guaranteed that this will happen; a return to all positive dot products is not possible.

At this point all data points stored are written out in cross section form. The numbering of these cross sections begins again with one, indicating the beginning of a new segment. The data sets written out are separated into cross sections just as they were stored, with

an appropriate count for the number of data points. After all stored data points have been written out, the cross section being processed is also written out, exactly as read in except that the cross section number is changed to be the one following the last stored cross section.

Encountering a cross section with data points yielding all negative dot products also changes the segmenting plane(s) that data points will be compared to. In this example, after processing the cross section with all negative dot products, data points read in for succeeding cross sections will not be compared to the segmenting plane separating the head and neck, but now the set of three segmenting planes separating the neck from the thorax will be used for this comparison. This set of segmenting planes will continue to be used until another cross section is encountered giving all negative dot products, at which point the reference will again be switched to the next segmenting plane down.

This process outlined for the separation of data points belonging to the head from those belonging to the neck is continued on downward through the TIRR head-trunk segment. When complete, the program proceeds to process the TIRR arm and leg segments in a similar fashion. Many of the segmenting planes encountered will be horizontal. There is no overlap between segments where separation is performed by a horizontal plane. Because of this, no cross sections will be encountered with data points yielding both positive and negative dot products for this type of segmentation: in one cross section all data points will have positive dot products, and in the next cross section all dot products computed will be negative. In these cases no data points will be stored. The cross section with all negative dot products will be the first cross section of the next segment, and will be written out exactly as read in, with a cross section number of one.

One other deviation from the general pattern occurs when the last segment of any of the TIRR segments is encountered (i.e., the pelvis, either of the hands, or either of the feet). At this point there is no longer any segmenting plane to compare data points to.

All cross sections belonging to one of these last segments are simply written out as read in, changing only the cross section number.

After this algorithm has passed through all cross sections of all five TIRR segments, the data set has successfully been divided into 17 segments. Program SGMNTS at this point also writes out the total number of cross sections per segment, as an aid to the subsequent processing to be performed by program FLAPS.

2.2 PROGRAM FLAPS

Program FLAPS separates out data points describing the surface of the left shoulder flap, right shoulder flap, left hip flap, and right hip flap (see Figures 4a, b, and c) from the data output by program SGMNTS. The data output from program SGMNTS has data points belonging to the two shoulder flaps combined with the thorax data points, and those belonging to the hip flaps combined with pelvis data points. Data in the output of program SGMNTS associated with other segments requires no processing at this point, thus program FLAPS ignores these portions of the data, reading them in and writing them back out, unchanged.

Observation 1 made in conjunction with the description of program SGMNTS states that any one cross section could contain data points belonging to at most one segment. The processing to be performed by program FLAPS, however, requires this program to look at cross sections that are to be separated into three different segments (i.e., there are cross sections that will be separated into left shoulder flap, thorax, and right shoulder flap, as well as cross sections to be separated into left hip flap, pelvis, and right hip flap).

In order to solve this problem and still make use of Observation 1, program FLAPS is run twice. The first time it is run, it separates out data points belonging to the flaps on the left side of the body, leaving the right shoulder flap part of the thorax and the right hip flap part of the pelvis. Program FLAPS is then run a second time, processing the data output from its first run. On this

second pass, flaps on the right side of the body are separated from the thorax and pelvis. The thorax and pelvis being examined in this second run of FLAPS no longer contain data points belonging to flaps on the left side of the body; rather, these data points have been listed by the first run of FLAPS as separate segments, and are simply skipped over on this second run, as are all other segments not requiring processing.

Observation 2 made in the discussion of program SGMNTS was that no segment could be both above and below another segment (assuming they were both to be separated out from the same TIRR segment). This observation can still be made for separating one hip flap at a time from the pelvis. However, when separating a shoulder flap from the thorax, this observation does not hold. The resulting thorax (minus flap) is both above and below the separated flap. Observation 2 is very useful when separating one segment (such as the TIRR head-trunk segment) into numerous segments (head, neck, thorax, abdomen, pelvis). In the case of program FLAPS, however, the thorax data set is only to be separated into two segments on each run of program FLAPS.

Since the thorax is only to be divided into two segments, the changes to be made in approach are only minor, even though Observation 2 does not apply. As each cross section of the combined thorax and shoulder flap is examined (top to bottom), dot products are computed for each data point, as in program SGMNTS. Cross sections yielding all positive or combinations of positive and negative dot products are handled in the same manner as they were in program SGMNTS. The difference is that a cross section yielding all negative dot products is never encountered. After some number of cross sections with dot products of mixed signs have passed, cross sections will be again encountered yielding only positive dot products (i.e., all data points again belong to the thorax minus shoulder flap segment). These cross sections continue to be processed, until the last cross section of the combined thorax-shoulder flap segment is processed. At this point, all stored data points are written out in cross sections, forming a (left or right, depending upon which run of program FLAPS) shoulder flap segment.

After the data set has passed through program FLAPS twice, it is completely segmented, and consists of 21 segments. As was done by program SGMNTS, program FLAPS writes out an updated list of the total number of cross sections per segment as the final process of each run, making this information available for the second run of FLAPS as well as for program POLISH.

2.3 PROGRAM POLISH

The data set received by program POLISH has been completely separated, and thus program POLISH performs no separation of data. Program POLISH does perform three tasks: it prepares a heading for the final form of the data, it combines the shoulder flaps with their respective upper arm segments, and it creates two additional cross sections of data points. Like program FLAPS, program POLISH leaves much of the data unchanged. Such data is simply read in and written back out.

2.3.1 Combining Shoulder Flaps with Upper Arms

The work done previously by McConville et al. (1980) defines a total of 19 body segments, not the 21 output by FLAPS. The difference here is that the shoulder flaps are not recognized as distinct segments by McConville. The set of 19 segments includes the shoulder flap area of the body as part of the upper arm (see Figure 3), but not as part of the thorax as they were originally recorded in the TIRR data. Thus, the separation of the shoulder flap from the thorax by program FLAPS was necessary so that this data set could be combined with upper arm data at a later point in time.

The separation between a shoulder flap and its corresponding upper arm is a horizontal plane, and thus there are no overlapping cross sections between the two. When program POLISH encounters the two shoulder flap segments, it reads the data pertaining to these segments in and stores this data. The data for each shoulder flap is then written back out immediately preceding the data for the corresponding upper arm segment. The cross section numbers are then changed for the cross sections in the upper arm segments, so

that their numbering is consecutive with that begun in the shoulder flap areas. This process combines each shoulder flap with its corresponding upper arm segment.

2.3.2 Establishing Additional Cross Sections

The inertial analyses to be performed on the body surface data require that segments have data points on the extreme parts of each segment. This was the reason for adding two data points on the intersection between a cross section and a segmenting plane for overlap areas: to define the boundaries of these segments. Analogously, a cross section is added by program POLISH to the bottom of the thorax, the top and bottom of the abdomen, and the top of the pelvis, firmly defining the boundaries of these segments.

Program POLISH actually creates only two new cross sections: one lies in the plane separating the thorax from the abdomen, and the other lies in the plane separating the abdomen from the pelvis. The cross section created between the thorax and the abdomen is constructed to be the weighted average of the bottom-most cross section of the throax and the topmost cross section of the abdomen. Similarly, the cross section created between the abdomen and the pelvis is constructed to be the weighted average of the bottom-most cross section of the abdomen and the topmost cross section of the pelvis. The weight factors used reflect the proximity of the two cross sections used in the average to the cross section being created. Details of the computations performed to construct these two cross sections are given in Appendix B.

After the cross section is created between the thorax and the abdomen, it is written out immediately following the data for the old bottom-most cross section of the thorax. Its cross section number being one greater than the old bottom-most cross section, making the created cross section the new bottom-most cross section of the thorax. This created cross section is then written out a second time with a cross section number of one, making it the first cross section of the abdomen. All original cross sections of the abdomen are then written out with their cross section numbers increased by one. The cross

section created between the abdomen and the pelvis is then written out twice. The first time it serves as bottom-most cross section of the abdomen, and the second time as first cross section of the pelvis, with all cross section numbers appropriately adjusted.

2.3.3 Preparing a Heading for the Data

Program POLISH performs one other major task: the creation of a header for the final form of the data. This header consists of the identification number of the subject, a list of segment names with the number of cross sections in each of these segments, and a list of the names of the 76 anthropometric landmarks along with the coordinates of these landmarks. The subject number is simply the sequence number of the data as recorded by TIRR (i.e., data for subjects 1 through 59).

This task (preparation of the header) is actually performed first, but when it is done consideration must be made of the changes which will be made to the data by the remainder of program POLISH. That is, the number of cross sections associated with some of the segments will be altered by program POLISH. In particular, the number of cross sections associated with either of the upper arm segments after POLISH is run is equal to the number of cross sections in that upper arm prior to processing by POLISH, plus the number of cross sections in the shoulder flap that it is combined with. Also, the number of cross sections associated with both the throax and pelvis is increased by one, and the number associated with the abdomen is increased by two, in order to reflect the cross sections that are created by POLISH.

Once program POLISH has completed execution the data set for a subject is in a completed form which is ready for analysis of inertial properties. A heading is available to provide useful information to any program performing such analysis. The entire data set is completely separated into 19 segments, with clear definitions of the boundaries of all segments.

2.4 CONCLUSION

Programs SGMNTS, FLAPS, and POLISH were used to prepare the TIRR data for processing by the analysis routines discussed in Section 3. The output of program POLISH was directly usable by the analysis routines for all but three of the data sets. Special treatment was required for these data sets.

The forty-eighth data set contained one data point in the last cross section of the left foot, that was erroneously recorded by TIRR. This data point was over 60 cm to the left of any other point in the cross section. For that reason it was removed.

The entire first cross section of the left upper arm of the forty-first data set was also removed. This cross section contained three data points one of which was originally part of the TIRR head-trunk segment (and later the left shoulder flap). The other two points were added by program FLAPS (by the method described in Appendix A). The one original point was co-planar with the segmenting plane separating the left shoulder flap from the thorax. Thus, the two added points were co-linear with this point, which resulted in the first cross section of the left upper arm being one dimensional, instead of two. The method used to compute inertial properties from the stereophotometric data, require calculation of the area of each cross section, which is not possible for a one dimensional figure. The simplest solution to this problem was to remove this cross section, which was done.

The thirty-seventh data set contains a cross section which lies in the segmenting plane, separating the abdomen from the pelvis. Thus, there was no need to create a cross section here. The one that was created was removed (both as the last cross section of the abdomen and as the first cross section of the pelvis) and the existing cross section was duplicated, so that it could serve as the bottom-most cross section of the abdomen, and the topmost cross section of the pelvis.

SECTION 3

ANALYSES PERFORMED ON SEGMENTED DATA

The development of a computer program to calculate inertial properties for each of the 19 segments shown in Figure 3 was performed by members of the AFAMRL/BBM. The resulting computer program was entitled IMPED. Work done under this contract (F33615-78-C-0504) provided further analysis of both the segmented data and the results obtained from the inertial analysis. The computer routines to do this further analysis took the form of subroutines, which were appended to IMPED. Thus running the combined program produced a very detailed analysis of the segmented data. Results of the analysis for a typical data set are listed in Appendix I.

The specific analyses performed are listed and detailed in Paragraphs 3.1 to 3.6. A listing of the subroutines used to perform these analyses may be found in Appendix H. Also in Appendix H is a listing of the block data area used to supply data to these subroutines.

3.1 READING OF HEADER AND CONVERSION TO GLOBAL AXES

Subroutine RWTBL1 was written to read in the header prepared for the data sets by program POLISH (see Paragraph 2.3). The data read in is stored so that it is available to the calling program, IMPED, as well as other subroutines written under this contract. Subroutine RWTBL1 also determines the transformation necessary to convert anthropometric landmarks and body surface data points to the global axis system, used by McConville et al. (1980).

The axis system used by TIRR in preparation of the stereophotometric data and throughout the segmentation process was based entirely upon the room in which the photographs to be digitized were taken. Subjects were placed in the room so that roughly X pointed to the right of each subject, Y to the front, and Z upward. The global axis system, defined by McConville et al. (1980), like the system used by TIRR used the standing surface as the XY plane with Z upward. The Y axis of the global system was defined by the projection of the line segment connecting the left and right anterior superior iliac spines

(ASIS) onto the standing surface, with positive Y pointing towards the left side of the body. The origin of the global system is the midpoint of this projection. The positive global X axis points towards the front of the body, making this a right handed system.

Subroutine RWTBL1 computes the transformation necessary to convert coordinates from the axis system used by TIRR to the global system of McConville. RWTBL1 then applies this transformation to each of the landmarks, writing the resulting coordinates out in the form shown in Table 1 of Appendix I. The data necessary for the transformation is also stored so that it may be used by the calling program, IMPED, to convert the coordinates of cross section data points to the global axis system, as these coordinates are read in.

3.2 CALCULATION OF INERTIAL PROPERTIES FOR COMBINED SEGMENTS

In addition to computing results (inertial properties, etc.) for the 19 segments shown in Figure 3, results are also computed for six additional segments, which are specified combinations of the 19 elementary segments. These six additional segments are listed and defined in Table 3. Subroutine COMBMI controls the sequencing of computations necessary to compute inertial properties for these combined segments from the inertial properties of their component segments. These computations are based upon the parallel axis theorem. The results are stored temporarily to be written out at a later time.

3.3 LOCATING THE ANATOMICAL AXIS SYSTEM

For each body segment (including the combined segments) an anatomical axis system is defined. The definitions are based upon subsets of the 76 anthropometric landmarks located on or near the associated segment. Because anatomical axis systems are defined in this way, their orientation varies with the orientation of the associated segment. Thus, by measuring quantities relative to an anatomical axis system, the effect due to subject-to-subject variation of segment orientation is at least minimized, if not eliminated.

TABLE 3
COMBINED SEGMENTS - LISTING AND DEFINITION

BODY SEGMENT	COMPOSED OF SEGMENTS
Right Forearm Plus Hand	Right Forearm Right Hand
Left Forearm Plus Hand	Left Forearm Left Hand
Right Thigh	Right Hip Flap Right Thigh Minus Flap
Left Thigh	Left hip Flap Left Thigh Minus Flap
Torso	Thorax Abdomen Pelvis
Total Body	All Segments

Anatomical axis system definitions take the form:

XY plane - A, B, C

YZ plane - D, E

XZ plane - F

where A, B, C, D, E, and F are anthropometric landmarks. These definitions may be interpreted as saying that the plane defined by the three points, A, B, C, contains the X and Y anatomical axes. A second plane perpendicular to this first one, and containing the points D and E, also contains the anatomical Y and Z axes. The plane containing the X and Z anatomical axes is perpendicular to these first two planes and also contains the point F. This is a sufficient definition to locate the origin of the system and the X, Y, Z axes, but not their positive or negative directions. Adding the conventions that Z positive will be the direction most nearly upward, X positive the direction most nearly forward, and Y positive the direction most nearly pointing to the subject's left (the axis systems are defined so that there will be no ambiguity in applying these conventions) completely defines these axis systems.

The XY, YZ, and XZ planes may be interchanged in the actual definitions indicating the same interchanges in the interpretation. These definitions are listed in Table 4. The details of the computations necessary to locate the origin and determine the direction cosines of each anatomical axis system, relative to the global axis system, are given in Appendix C. The subroutine written to control the computation of the anatomical axis system locations has been named ANATOM. Typical results of running this subroutine are given in Tables 5 and 6 of Appendix I.

3.4 DETERMINATION OF THE PRINCIPAL AXIS SYSTEM

In addition to the global and anatomical axis system a third set of axis systems is defined, the principal axis systems. A principal axis system is defined for each segment based upon the inertial properties of that segment. The principal axis system for a segment has its origin at the segment's center of gravity and its X, Y, Z

TABLE 4

DEFINITION OF ANATOMICAL AXIS SYSTEMS

SEGMENT	BI-AXIS PLANE	LANDMARK
Head	XY	Right Tragion
		Left Tragion
		Right Infraorbitale
	YZ	Right Tragion
		Left Tragion
	XZ	Sellion
Neck	XZ	Mid Thyroid Cartilage
		Cervicale
		Suprasternale
	XY	Mid-Point Between Left and Right Clavicale
		Cervicale
	YZ	Cervicale
Thorax	XZ	Suprasternale
		Cervicale
		10th Rib Mid-Spine
	YZ	Cervicale
		10th Rib Mid-Spine
	XY	10th Rib Mid-Spine
Abdomen	XY	Left 10th Rib
		Right 10th Rib
		10th Rib Mid-Spine
	YZ	Left 10th Rib
		Right 10th Rib
	XZ	10th Rib Mid-Spine
Pelvis	YZ	Left ASIS
		Right ASIS
		Symphysion
	XY	Left ASIS
		Right ASIS
	XZ	Posterior Superior Iliac Mid-Spine
Right Upper Arm	YZ	Right Acromiale
		Right Medial Humeral Epicondyle
		Right Lateral Humeral Epicondyle
	XZ	Right Acromiale
		Right Lateral Humeral Epicondyle
	XY	Right Acromiale
Right Forearm	YZ	Right Ulnar Styloid
		Right Radial Styloid
		Right Radiale
	XZ	Right Ulnar Styloid
		Right Radiale
	XY	Right Radiale
Right Hand	YZ	Right Dactylion
		Right Metacarpale II
		Right Metacarpale V
	XY	Right Metacarpale II
		Right Metacarpale V
	XZ	Right Metacarpale III
Left Upper Arm	YZ	Left Acromiale
		Left Medial Humeral Epicondyle
		Left Lateral Humeral Epicondyle
	XZ	Left Acromiale
		Left Lateral Humeral Epicondyle
	XY	Left Acromiale
Left Forearm	YZ	Left Ulnar Styloid
		Left Radial Styloid
		Left Radiale
	XZ	Left Ulnar Styloid
		Left Radiale
	XY	Left Radiale
Left Hand	YZ	Left Dactylion
		Left Metacarple II
		Left Metacarpale V
	XY	Left Metacarpale II
		Left Metacarpale V
	XZ	Left Metacarpale III
Right Hip Flap	YZ	Right Trochanterion
		Right Lateral Femoral Condyle
		Right Medial Femoral Condyle
	XZ	Right Laterial Femoral Condyle
		Right Trochanterion
	XY	Right Trochanterion
Right Thigh Minus Flap		Same as Right Hip Flap
Right Calf	YZ	Right Tibiale
		Right Sphyrion
		Right Lateral Malleolus
	XZ	Right Sphyrion
		Right Tibiale
	XY	Right Tibiale
Right Foot	XY	Right Metatarsal I
		Right Metatarsal V
		Right Posterior Calcaneous
	XZ	Right Toe II
		Right Posterior Calcaneous
	YZ	Right Metatarsal I
Left Hip Flap	YZ	Left Trochanterion
		Left Lateral Femoral Condyle
		Left Medial Femoral Condyle
	XZ	Left Lateral Femoral Condyle
		Left Trochanterion
	XY	Left Trochanterion
Left Thigh Minus Flap		Same as Left Hip Flap
Left Calf	YZ	Left Tibiale
		Left Sphyrion
		Left Lateral Malleolus
	XZ	Left Sphyrion
		Left Tibiale
	XY	Left Tibiale
Left Foot	XY	Left Metatarsal I
		Left Metatarsal V
		Left Posterior Calcaneous
	XZ	Left Toe II
		Left Posterior Calcaneous
	YZ	Left Metatarsal I
Right Forearm Plus Hand		Same as Right Forearm
Left Forearm Plus Hand		Same as Left Forearm
Right Thigh		Same as Right Hip Flap
Left Thigh		Same as Left Hip Flap
Torso		Same as Pelvis
Total Body		Same as Pelvis

axes coincide with the three directions associated with the principal moments of inertia. Additionally the principal axes are to be a right handed system. Assigning a right handed axis system to three orthogonal directions can be done in one of 24 ways. The actual assignment of axes chosen is the one that has the closest alignment with that segment's anatomical axis system. Once this principal axis system has been defined, the already-calculated principal moments of inertia can be assigned the names, X, Y, and Z principal moments, accordingly. The details of the algorithm used to fix the principal axis system to one of the 24 possibilities are listed in Appendix D. Subroutine ALIGN, listed in Appendix H implements this algorithm. With this process complete the principal moments of inertia and the direction cosines of the principal axis system are written out forming Tables 3 and 4, which are listed in Appendix I.

3.5 TABULATION OF HEIGHT VERSUS VOLUME

Interest has been expressed in the percentage of total body volume contained between two arbitrary horizontal planes. In order to provide this data, subroutine HTVSVL was written to control the computations necessary to produce a table of percent of body volume contained between the floor and a horizontal plane at specified heights. Table 15 of Appendix I gives results typical for this table. Details of the computations performed are given in Appendix E.

3.6 MISCELLANEOUS ROUTINES

Appendix H gives listings of all subroutines written under this contract which became a part of program IMPED. In addition to those mentioned there are subroutines to compute the coordinates of the landmarks, segment centers of gravity, and segment anatomical origins in each of the three (global, anatomical, and principal) axis systems. Also there are routines used to simplify the output of data in table form, and other activities necessary to produce the set of tables presented in Appendix I.

APPENDIX A

ADDITION OF DATA POINTS TO A CROSS SECTION

This appendix is an example illustrating the computations involved in examining a cross section. Computations such as those to be illustrated are carried out both in program SGMNTS and in program FLAPS. Procedures illustrated include computation of dot products and addition of two data points to the cross section. Data points used belong to a cross section in the overlap area between the head and the neck of the eleventh data set. Coordinates of data points used in this example are relative to the axis system used by TIRR (X and Y point approximately to the subject's right and front, respectively, and Z points upwards), and are measured in centimeters. The common Z coordinates of these data points is 153.95, their X, Y coordinates are listed in Table 5.

The normal to the plane separating the head from the neck is defined to be the cross product of two vectors both originating at the left gonion (L_{39}), one going to the right gonion (L_{40}), and the other to the nuchale (L_1). For the eleventh data set these landmark points have coordinates

$$L_{39} = (\ell_{39x}, \ell_{39y}, \ell_{39z}) = (41.50, 0.76, 153.10)$$

$$L_{40} = (52.69, 0.55, 153.16)$$

$$L_1 = (46.92, -9.20, 156.65)$$

which give the normal to be

$$N = (n_1, n_2, n_3) = (L_{40}-L_{39}) \times (L_1-L_{39}) = (0.148, 39.40, 110.3)$$

The segmenting plane is further defined to contain the left gonion. Thus when a data point (x_{ij}, y_{ij}, z_i), is compared to this segmenting plane, dot products are constructed to be

$$d = n_1(x_{ij}-\ell_{39x}) + n_2(y_{ij}-\ell_{39y}) + n_3(z_i-\ell_{39z}) .$$

TABLE 5

DATA POINTS USED IN APPENDIX A EXAMPLE

.148	39.399	118.314 = SEGMENTING PLANE NORMAL
41.50	.76	153.10 = PLANE DEFINITION PT.

153.95 = COMMON Z COORDINATE OF CROSS SECTION

POINT#	X	Y	DOT PRODUCT	SEGMENT
1	41.06	-1.59	1.114	HEAD
2	41.35	-3.08	-57.546	NECK
3	42.25	-4.66	-119.666	NECK
4	43.23	-6.20	-180.196	NECK
5	45.00	-6.91	-207.908	NECK
6	47.35	-7.35	-224.896	NECK
7	49.42	-6.96	-209.224	NECK
8	50.91	-5.93	-168.423	NECK
9	52.10	-4.87	-126.483	NECK
10	52.95	-3.47	-71.199	NECK
11	53.26	-2.22	-21.904	NECK
12	53.61	1.61	129.048	HEAD
13	53.38	3.38	198.750	HEAD
14	52.16	5.69	297.462	HEAD
15	50.57	7.29	352.386	HEAD
16	48.70	8.45	397.813	HEAD
17	47.16	9.22	427.922	HEAD
18	45.21	8.96	417.390	HEAD
19	43.42	7.74	369.058	HEAD
20	42.23	6.69	327.513	HEAD
21	41.12	5.31	272.978	HEAD
22	40.68	3.29	193.326	HEAD
23	40.63	1.63	127.916	HEAD
24	40.63	1.63	127.916	HEAD

ADDED POINTS:

41.07	-1.62	153.95
53.31	-1.66	153.95

The results of the dot product computation for each data point in the cross section are shown in Table 5. Those with negative dot products are stored to be written out later as part of the neck segment, the remainder are written out immediately as part of the head segment.

Reading through the dot products in Table 5 from top to bottom there are two pairs between which the sign of the dot product changes. These are points number 1 and 2, and points number 11 and 12. In all cases of a cross section with data points belonging to two segments, there will be two places of sign change like this (based on the fact that data points are listed in order around the cross section), although in some cases to find both sign changes the list must be considered circular (i.e., the first data point must be considered to follow the last). For each of these pairs of points a line segment is constructed between the two members of the pair. At the intersections of the segmenting plane and each of these line segments the two points to be added to the cross section are located. This is shown graphically in Figure 5.

Consider two points (x_1, y_1, z_0) and (x_2, y_2, z_0) in some cross section, such that they are adjacent points in the cross section and their resulting dot products are opposite in sign. All points on the line connecting these two points may be expressed by

$$\left(x, \left(\frac{y_1-y_2}{x_1-x_2}\right) (x-x_1) + y_1, z_0\right) \tag{A.1}$$

with x variable. Let the segmenting plane they are being compared to have a normal vector with components (n_1, n_2, n_3) and defining landmark (ℓ_x, ℓ_y, ℓ_z). Then all points (x, y, z) lying in this plane satisfy

$$n_1(x - \ell_x) + n_2(y-\ell_y) + n_3(z-\ell_z) = 0 . \tag{A.2}$$

In order to find the intersection between the line (A.1) and the plane (A.2), (A.1) is substituted into (A.2).

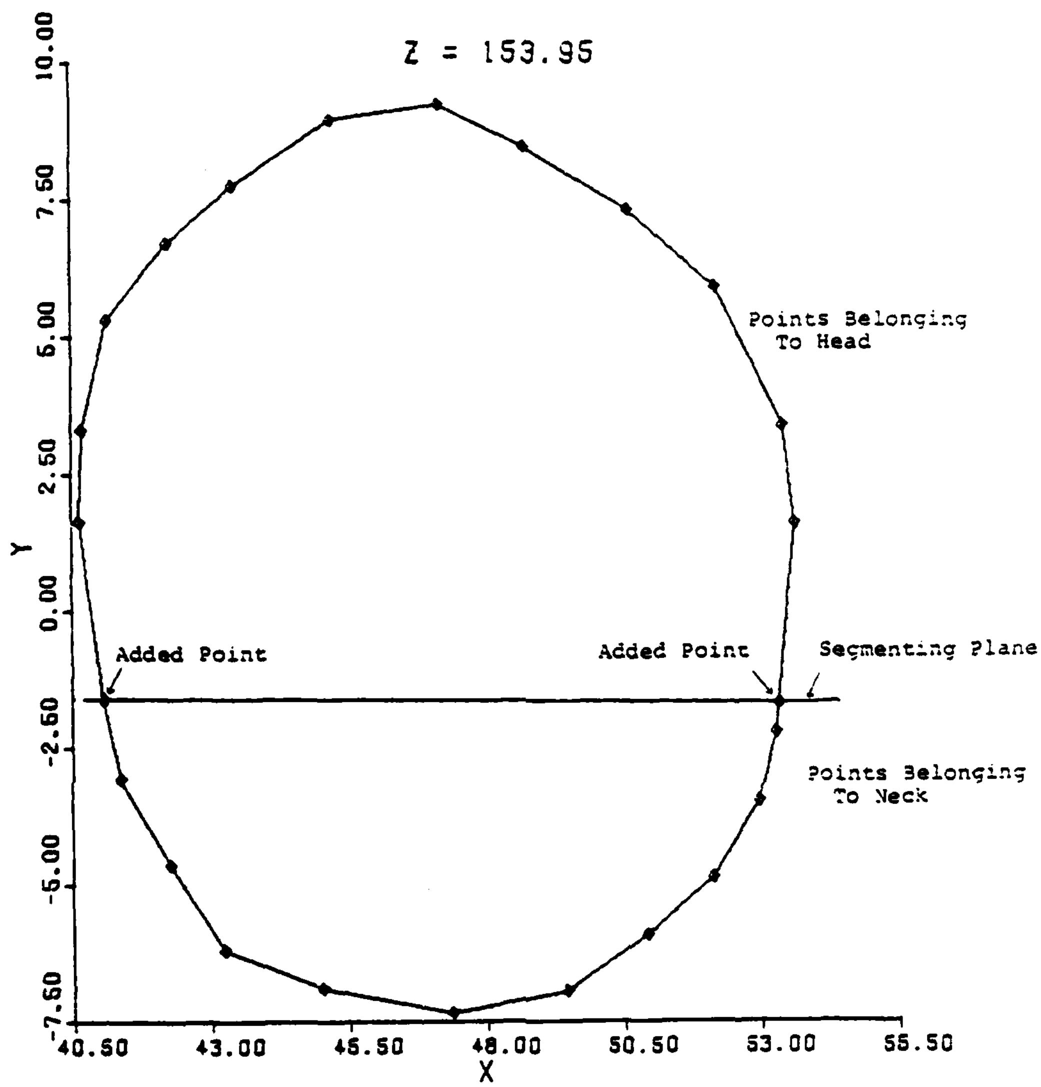


Figure 5. Addition of Data Points at Intersection Between Segmenting Plane and Horizontal Plane Containing Cross Section.

$$n_1\left(x-\ell_x\right) + n_2\left(\left(\frac{y_1-y_2}{x_1-x_2}\right)\left(x-x_1\right) + y_1-\ell_y\right) + n_3\left(z_0-\ell_z\right) = 0. \tag{A.3a}$$

Solving for x and simplifying gives

$$x = \frac{n_3(\ell_z-z_0)(x_1-x_2) + n_1\ell_x(x_1-x_2) + x_1n_2(y_1-y_2) + n_2(\ell_y-y_1)(x_1-x_2)}{n_1(x_1-x_2) + n_2(y_1-y_2)}. \tag{A.3b}$$

Note that since the segmenting plane passes between the two points, the denominator of A.3b will never be zero. The X coordinate of one of the points to be added is given by (A.3b); the Y and Z coordinates of this point may be found by substitution back into (A.1). The two points to be added to the cross section in the example are listed in Table 5.

APPENDIX B
CREATION OF A CROSS SECTION

Cross sections are created by program POLISH and added in the planes of segmentation separating the thorax from the abdomen and the abdomen from the pelvis. This appendix uses the creation of the cross section between the thorax and the abdomen of the eleventh subject's data set as an example of this process. As in Appendix A the coordinates used in this example are relative to the axis system used by TIRR and are measured in centimeters.

For subject 11, the data output by FLAPS lists the last cross section of the thorax as having Z coordinate, $Z_1 = 109.92$. The first cross section of the abdomen has Z coordinate, $Z_2 = 107.89$. The segmenting plane separating the thorax from the abdomen is a horizontal plane passing through the 10^{th} rib midspine landmark point, which has Z coordinate $Z_0 = 108.13$. The cross section to be created will have this Z coordinate. It will be constructed as an average of these other two cross sections. The coordinates of the data points contained in these two cross sections are listed in Table 6. The amount of influence each of these cross sections has in the averaging will be dependent upon its relative closeness to the cross section being created. Thus two weight factors are computed.

$$w_1 = \frac{Z_0 - Z_2}{Z_1 - Z_2} = 0.118 \qquad \text{and} \qquad w_2 = \frac{Z_1 - Z_0}{Z_1 - Z_2} = 0.882. \qquad \text{(B.1)}$$

These will be used throughout the computations.

All X coordinates of the last cross section of the thorax are averaged, as are the Y coordinates of this cross section, and the X and Y coordinates of the first cross section of the abdomen, yielding $\bar{X}_1$, $\bar{Y}_1$, $\bar{X}_2$, $\bar{Y}_2$ respectively. An overall center for these two cross sections (X_0, Y_0), then is computed as

$$X_0 = w_1\bar{X}_1 + w_2\bar{X}_2 \qquad \text{and} \qquad Y_0 = w_1\bar{Y}_1 + w_2\bar{Y}_2. \qquad \text{(B.2)}$$

TABLE 6

ORIGINAL AND CREATED DATA POINTS OF APPENDIX B EXAMPLE: RECTILINEAR AND POLAR COORDINATE FORM

	CROSS SECTION ABOVE				CROSS SECTION BELOW				CREATED CROSS SECTION			
CROSS SECTION Z COOR		109.92				107.89				108.13		
WEIGHT		.118				.882						
POINT#	X	Y	ANGLE	RADIUS	X	Y	ANGLE	RADIUS	ANGLE	RADIUS	X	Y
1	34.95	-4.90	-2.87	13.63	33.81	-3.98	-2.95	14.53	-2.95	14.42	33.95	-4.10
2	36.10	-7.15	-2.69	13.35	35.52	-6.83	-2.73	13.74	-2.75	13.81	35.30	-6.49
3	37.46	-8.68	-2.53	12.95	36.91	-8.13	-2.59	13.11	-2.56	12.94	37.25	-8.34
4	39.52	-9.80	-2.36	12.08	38.33	-8.81	-2.48	12.33	-2.37	11.74	39.64	-9.43
5	42.61	-10.28	-2.12	10.54	40.13	-9.53	-2.34	11.46	-2.18	10.37	42.13	-9.76
6	44.35	-10.19	-1.97	9.66	41.89	-9.70	-2.21	10.46	-1.99	9.06	44.30	-9.54
7	46.03	-3.55	-1.82	8.52	43.48	-9.64	-2.08	9.55	-1.80	8.02	46.25	-9.09
8	48.14	-9.90	-1.57	8.62	45.53	-9.15	-1.89	8.27	-1.61	7.98	47.76	-9.25
9	51.61	-10.34	-1.20	9.72	46.71	-9.02	-1.75	7.86	-1.42	8.46	49.35	-9.65
10	54.18	-10.02	-.96	10.65	49.77	-9.65	-1.37	8.53	-1.23	9.00	51.09	-9.77
11	55.89	-8.99	-.78	10.96	51.78	-9.67	-1.16	9.16	-1.04	9.73	53.00	-9.68
12	57.41	-7.88	-.62	11.42	53.50	-9.54	-.99	9.87	-.85	10.60	55.08	-9.25
13	58.98	-5.76	-.39	11.77	55.84	-8.97	-.78	10.91	-.66	11.48	57.16	-8.33
14	59.84	-3.73	-.21	12.00	58.14	-7.75	-.57	11.95	-.47	12.37	59.12	-6.89
15	59.99	-2.94	-.14	12.01	59.56	-6.57	-.43	12.63	-.28	12.86	60.45	-4.83
16	59.80	1.66	.25	12.07	60.44	-5.19	-.31	12.95	-.09	12.99	61.03	-2.44
17	58.46	4.56	.51	11.90	60.93	-3.65	-.18	13.05	.10	12.97	60.89	.02
18	56.83	5.96	.69	11.35	61.06	-3.09	-.14	13.09	.29	12.59	60.15	2.34
19	54.08	7.48	.91	11.08	60.77	.94	.17	12.87	.48	12.05	58.77	4.38
20	53.06	9.54	1.14	11.91	59.99	2.76	.33	12.57	.67	11.57	57.15	5.93
21	51.08	10.56	1.32	12.21	58.64	4.46	.50	12.01	.86	11.56	55.61	7.50
22	48.32	11.18	1.55	12.46	56.19	6.95	.79	11.55	1.05	11.32	53.99	9.07
23	44.25	10.92	1.88	12.79	54.28	8.92	1.03	11.93	1.24	12.10	51.98	10.16
24	42.22	10.17	2.04	12.87	52.45	9.96	1.20	12.06	1.43	12.41	49.78	11.01
25	40.23	8.70	2.24	12.71	49.72	11.04	1.44	12.43	1.62	12.67	47.41	11.37
26	38.23	6.25	2.49	12.41	46.67	11.35	1.68	12.71	1.81	12.69	45.03	11.03
27	36.20	4.22	2.71	13.10	43.86	10.71	1.91	12.72	2.01	12.88	42.67	10.40
28	34.81	1.58	2.93	13.59	41.27	9.87	2.12	13.07	2.20	13.05	40.46	9.30
29	34.32	-.15	3.06	13.82	39.31	8.29	2.31	12.99	2.39	12.87	38.73	7.54
30					37.71	6.40	2.50	12.92	2.58	12.95	37.15	5.66
31					35.05	3.37	2.80	13.85	2.77	13.61	35.42	3.70
32					33.64	1.32	2.96	14.68	2.96	14.55	33.78	1.39
33					33.54	.50	3.02	14.66	3.15	14.54	33.55	-1.37

ALL POLAR COORDINATES RELATIVE TO 46.89 -1.28

This pair of values will be used for transformation to polar coordinates, and, for this example, are listed in Table 6.

Ignoring Z coordinates and using (X_0, Y_0) as a center, polar coordinates are computed for each data point in the two cross sections. For later computations it is necessary that within each cross section, data is stored with increasing values of angle. Table 6 lists the polar coordinates of the data points, and is constructed so that angles are in ascending order. Figure 6a graphically shows the polar coordinate form of the data points in the last cross section of the thorax.

The next step performed in order to create a cross section between the thorax and abdomen is to fit a spline to both sets of polar coordinates. The fitting of a spline involves what can be an arbitrary decision about end point conditions of the data. Generally this takes the form of specifying the derivative the spline will take on at each end point. Since the data the spline is being fit to are the polar coordinates of data points that form a closed loop, in polar coordinate form the radius is a periodic function of angle, with period 2π. Making use of this fact, data points may be extended in either direction, thus lessening the effect of the chosen end conditions on the original portion of the data. As is shown in Figure 6b data points are extended one half period plus one point to the right and left of the original data, for the last cross section in the thorax. This same procedure is also applied to the first cross section of the abdomen. The extended data points for both are listed in Table 7.

Even though the data points have been extended to the left and the right, some values still must be used for the end conditions. These are computed by interpolating the last three and the first three (extended) data points of both cross sections with a parabola. For any one such set of three points (θ_1, r_1), (θ_2, r_2), (θ_3, r_3) the equation of the parabola through them is

$$r(\theta) = \frac{(\theta-\theta_2)(\theta-\theta_3)}{(\theta_1-\theta_2)(\theta_1-\theta_3)} r_1 + \frac{(\theta-\theta_1)(\theta-\theta_3)}{(\theta_2-\theta_1)(\theta_2-\theta_3)} r_2 + \frac{(\theta-\theta_1)(\theta-\theta_2)}{(\theta_3-\theta_1)(\theta_3-\theta_2)} r_3 \; . \tag{B.3}$$

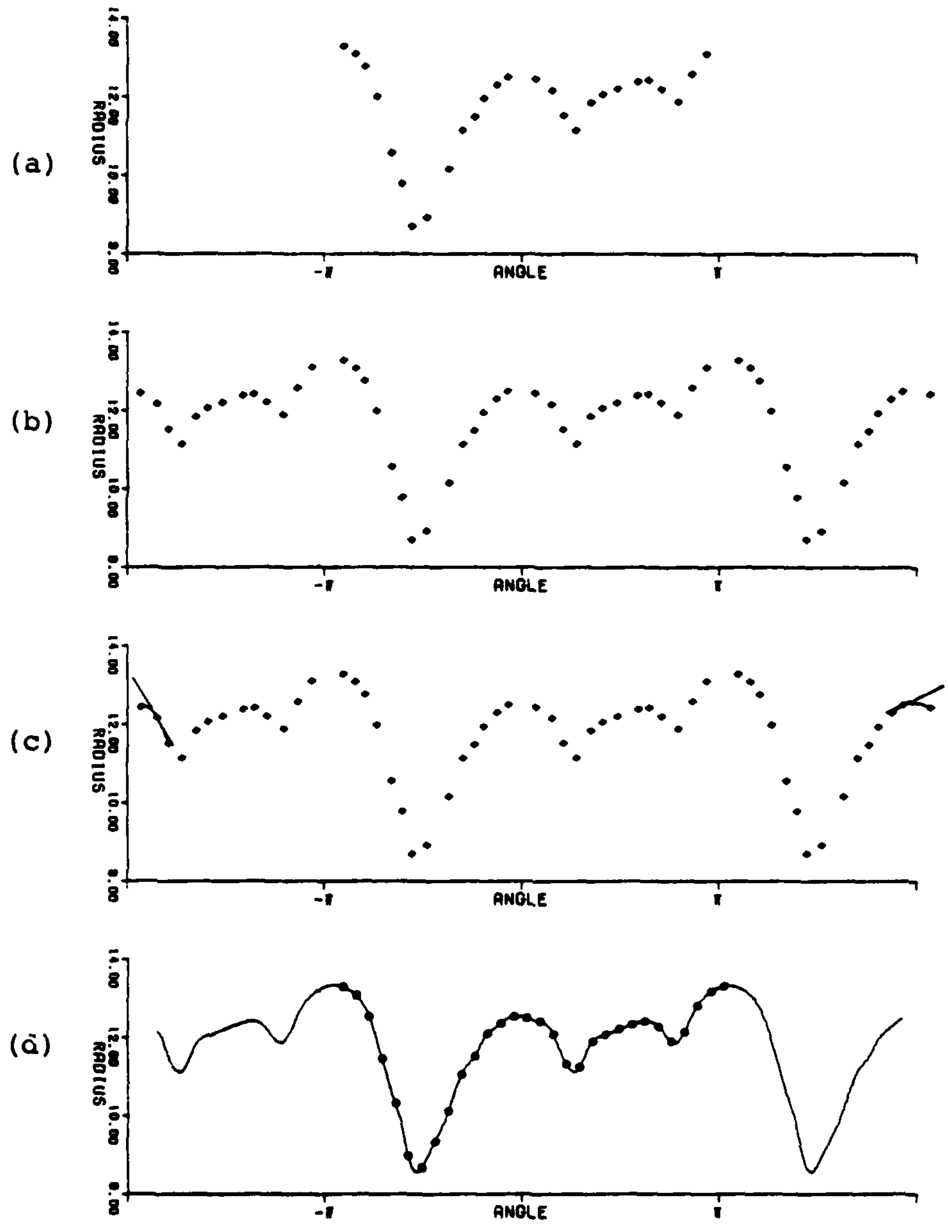


Figure 6. Successive Steps in the Creation of a Cross Section Between the Thorax and Abdomen of Subject 11.

(a) Polar coordinate form of data points in bottom-most cross section of thorax.
(b) Data points extended one-half period plus one point to the left and right.
(c) Parabolas and their tangents used to determine end conditions of the spline.
(d) Spline fit to data and new data points determined by spline.

TABLE 7

EXTENDED FORM OF DATA POINTS OF APPENDIX B EXAMPLE, AND END POINT CONDITIONS USED IN FITTING SPLINE

CROSS SECTION ABOVE

PT#	ANGLE	RADIUS	PT#	ANGLE	RADIUS
1	-6.42	12.01	31	.25	12.07
2	-6.04	12.07	32	.51	11.90
3	-5.77	11.90	33	.69	11.35
4	-5.59	11.35	34	.91	11.08
5	-5.37	11.08	35	1.14	11.91
6	-5.14	11.91	36	1.32	12.21
7	-4.96	12.21	37	1.55	12.46
8	-4.73	12.46	38	1.88	12.79
9	-4.41	12.79	39	2.04	12.87
10	-4.24	12.87	40	2.24	12.71
11	-4.05	12.71	41	2.49	12.41
12	-3.79	12.41	42	2.71	13.10
13	-3.57	13.10	43	2.93	13.59
14	-3.35	13.59	44	3.06	13.82
15	-3.22	13.82	45	3.41	13.63
16	-2.87	13.63	46	3.60	13.35
17	-2.69	13.35	47	3.75	12.95
18	-2.53	12.95	48	3.92	12.08
19	-2.36	12.03	49	4.17	10.54
20	-2.12	10.54	50	4.31	9.65
21	-1.97	9.66	51	4.47	8.52
22	-1.82	8.52	52	4.72	8.62
23	-1.57	8.62	53	5.08	9.72
24	-1.20	9.72	54	5.32	10.65
25	-.96	10.65	55	5.50	10.96
26	-.78	10.96	56	5.67	11.42
27	-.62	11.42	57	5.89	11.77
28	-.39	11.77	58	6.08	12.00
29	-.21	12.00	59	6.14	12.01
30	-.14	12.01	60	6.53	12.07

CROSS SECTION BELOW

PT#	ANGLE	RADIUS	PT#	ANGLE	RADIUS
1	-6.47	13.05	35	-.14	13.09
2	-6.42	13.09	36	.17	12.87
3	-6.11	12.87	37	.33	12.57
4	-5.96	12.57	38	.50	12.01
5	-5.78	12.01	39	.79	11.55
6	-5.49	11.55	40	1.03	11.93
7	-5.26	11.93	41	1.20	12.06
8	-5.08	12.06	42	1.44	12.43
9	-4.84	12.43	43	1.68	12.71
10	-4.60	12.71	44	1.91	12.72
11	-4.37	12.72	45	2.12	13.07
12	-4.16	13.07	46	2.31	12.99
13	-3.97	12.99	47	2.50	12.92
14	-3.78	12.92	48	2.80	13.85
15	-3.48	13.85	49	2.96	14.68
16	-3.32	14.68	50	3.02	14.66
17	-3.26	14.66	51	3.33	14.53
18	-2.95	14.53	52	3.56	13.74
19	-2.73	13.74	53	3.69	13.11
20	-2.59	13.11	54	3.80	12.33
21	-2.48	12.33	55	3.94	11.46
22	-2.34	11.46	56	4.08	10.46
23	-2.21	10.46	57	4.21	9.55
24	-2.08	9.55	58	4.40	8.27
25	-1.89	8.27	59	4.54	7.86
26	-1.75	7.86	60	4.91	8.53
27	-1.37	8.53	61	5.13	9.16
28	-1.16	9.16	62	5.29	9.87
29	-.99	9.87	63	5.50	10.91
30	-.78	10.91	64	5.71	11.95
31	-.57	11.95	65	5.85	12.63
32	-.43	12.63	66	5.98	12.95
33	-.31	12.95	67	6.10	13.05
34	-.18	13.05	68	6.14	13.09

DERIVATIVES:

	CROSS SECTION ABOVE	CROSS SECTION BELOW
AT LEFT END POINT	-.316	.689
AT RIGHT END POINT	.183	.871

Evaluating the derivative of this parabola then at θ_2 gives

$$r'(\theta_2) = 2\theta_2\left(\frac{r_1}{(\theta_1-\theta_2)(\theta_1-\theta_3)} + \frac{r_2}{(\theta_2-\theta_1)(\theta_2-\theta_3)} + \frac{r_3}{(\theta_3-\theta_1)(\theta_3-\theta_2)}\right)$$

$$- \left(\frac{(\theta_2+\theta_3)r_1}{(\theta_1-\theta_2)(\theta_1-\theta_3)} + \frac{(\theta_1+\theta_3)r_2}{(\theta_2-\theta_1)(\theta_2-\theta_3)} + \frac{(\theta_1+\theta_2)r_3}{(\theta_3-\theta_1)(\theta_3-\theta_2)}\right). \qquad \text{(B.4)}$$

Using this equation, derivatives of parabolas through all four sets of three points may be computed, with the point intermediate of the other two, in each case, supplying the values for (θ_2, r_2). The results of these computations are given in Table 7 as well as graphically, for the last cross section of the thorax only, in Figure 6c. Splines may now be fit to each set of data, first deleting the two extreme end points of each cross section, and then supplying the computed values for derivatives of the parabolas, as the first derivative of each end point of the splines.

A set of angles, $\{\theta_i\}$, are next constructed. The first angle in this set is constructed to be the weighted average of the first angle in each cross section. The number of angles in this set, N_0, is set to be the weighted average of the number of data points in the two cross sections

$$N_0 = W_1N_1 + W_2N_2$$

where N_0 is rounded to the nearest integer. The remainder of this set of N_0 angles is then constructed from the recursive relation

$$\theta_i = \theta_{i-1} + \frac{2\pi}{N_0}, \qquad i = 2, 3, \ldots N_0$$

These angles will be used in the polar coordinates of the data points of the created cross section, and are listed in Table 6.

Both splines are then evaluated at each one of the angles in this set, resulting in two sets of radii $\{r_i^1\}$ and $\{r_i^2\}$, the former set being evaluations of the spline corresponding to the last cross section of the thorax, and the latter set from the spline for the first cross section of the abdomen. The set of points (θ_i, r_i^1) is illustrated in Figure 6d, along with the spline used to compute the r_i^1.

The weighted average is then taken of these two sets of radii, component-wise, resulting in a third set of radii $\{r_i^0\}$. That is

$$r_i^0 = w_1 r_i^1 + w_2 r_i^2 , \qquad i = 1, \ldots, N_0$$

The ordered pairs (θ_i, r_i^0) then form the polar coordinates of the cross section being created, and for the example are listed in Table 6. Converting these polar to rectilinear coordinates, relative to (X_0, Y_0) then supplies the data points for the new cross section.

This resulting data set is then written out twice, once as the last cross section of the thorax and again as the first cross section of the abdomen. The relationship between the created cross section and the two cross sections used in its creation is shown in Figure 7.

A process analogous to the one outlined is followed in order to create a cross section between the abdomen and the pelvis.

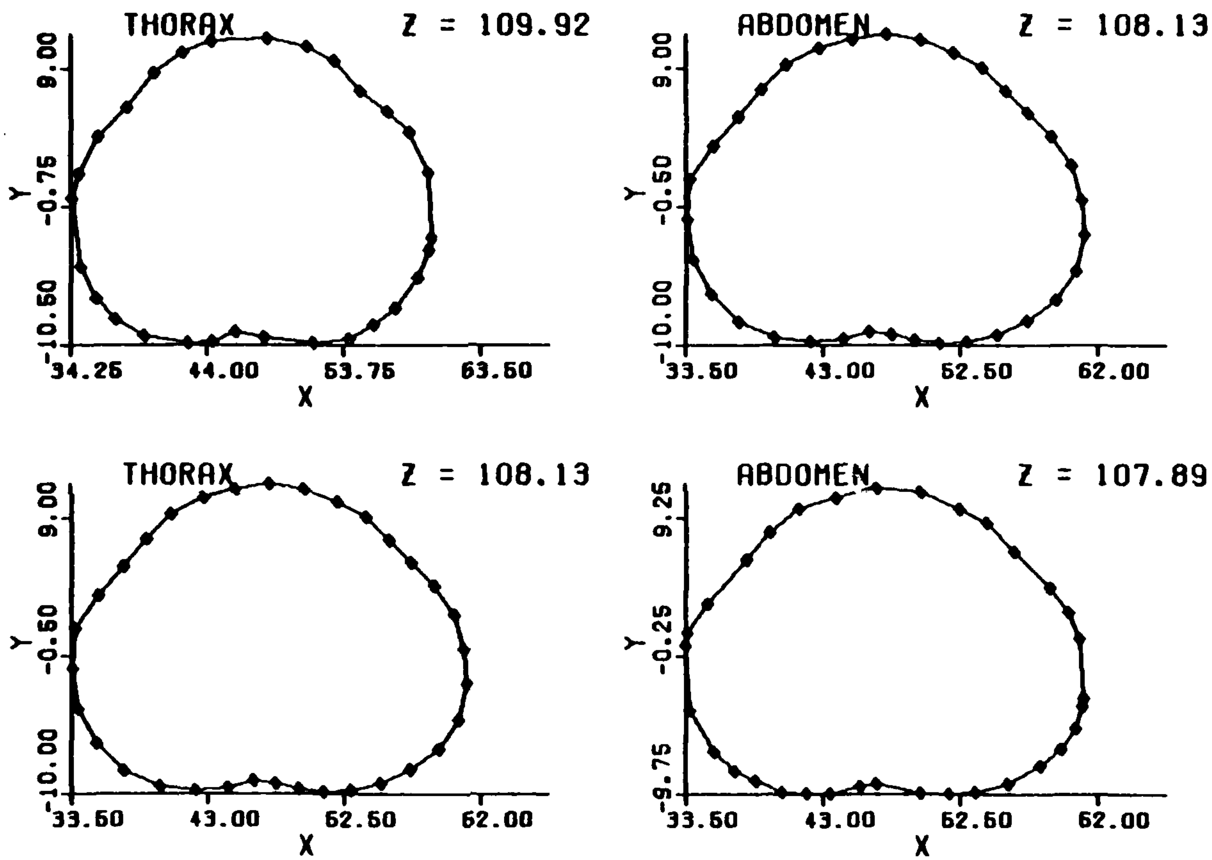


Figure 7. Cross Section Created Between Thorax and Abdomen (Z=108.13) for Subject 11; Cross Section Above (Z=109.92); and Cross Section Below (Z=107.89).

APPENDIX C

DETERMINATION OF ORIGIN AND DIRECTION COSINES OF SEGMENT ANATOMICAL AXIS SYSTEMS

As can be seen in Table 4 none of the anatomical axis system definitions use six unique landmarks to define the anatomical axis systems, but instead repeat some landmarks. For generality, though, no assumptions about repeated points will be made in the development of equations to locate the anatomical axis system; rather, each of the six points will be treated as unique.

Notation to be used in the development of these equations includes using the capital letters A-G (including G_1, G_2) to denote points in three space. The coordinates of these points, measured in the global axis system, are denoted by lower case letters with the subscripts 1 through 3. For example $A = (a_1, a_2, a_3)$. In particular the letters A through F are the anthropometric landmarks used to define the anatomical axis system. N_{xy}, N_{yz}, and N_{xz} denote the normal vectors to the anatomical XY, YZ, and XZ planes respectively. The components of these vectors are denoted by subscripts of 1, 2, 3 for first, second, and third component, respectively. For example $N_{xy} = (N_{xy_1}, N_{xy_2}, N_{xy_3})$.

Let a general anatomical axis system be defined as

XY	A, B, C
YZ	D, E
XZ	F

From the definition the following statements may be made:

- the anatomical XY plane contains the points A, B, C
- the anatomical YZ plane contains the points D, E
- the anatomical XZ plane contains the point F.

The result is immediately obtainable that

$$N_{xy} = \frac{(A-C) \times (B-C)}{\|(A-C) \times (B-C)\|} .$$

Since N_{yz} is normal to N_{xy} and to any vector in the YZ plane, the following equations result:

$$N_{yz} \cdot N_{xy} = 0 , \tag{C.1}$$

$$N_{yz} \cdot (D-E) = 0 . \tag{C.2}$$

From (C.1) the function g is defined as

$$g(N_{yz_2}, N_{yz_3}) = N_{yz_1} = \frac{N_{yz_2}N_{xy_2} + N_{yz_3}N_{xy_3}}{-N_{xy_1}} .$$

(C.1) and (C.2) may be solved simultaneously yielding the function f

$$f(N_{yz_3}) = N_{yz_2} = \frac{N_{yz_3}[N_{xy_3}(d_x-e_x) + N_{xy_1}(e_z-d_z)]}{[N_{xy_2}(e_x-d_x) + N_{xy_1}(d_y-e_y)]} .$$

Consider then the vector $(g(f(z), z), f(z), z)$, for any value of $z \neq 0$. This vector has the same direction as N_{yz}, changing z changes only the magnitude of this vector and not its direction (since f and g are linear functions). Then there exists z_0 such that $\|(g(f(z_0), z_0), f(z_0), z_0)\| = 1$. Using z_0 then

$$N_{yz} = (g(f(z_0), z_0), f(z_0), z_0) .$$

Next let G be any point on the anatomical Y axis. Then

$$(G-D) \cdot N_{yz} = 0 \tag{C.3}$$

$$(G-C) \cdot N_{xy} = 0 . \tag{C.4}$$

From (C.4) the function h_1 is defined as

$$h_1(g_y, g_z) = g_x = \frac{C \cdot N_{xy} - N_{xy_2} g_y - N_{xy_3} g_z}{N_{xy_1}} .$$

(C.3) and (C.4) may be solved simultaneously yielding the function h_2

$$h_2(g_z) = g_y = \frac{\left[C \cdot N_{xy} - \left(\frac{N_{xy_1}}{N_{yz_1}}\right) D \cdot N_{yz}\right] - g_z \left[N_{xy_3} - \frac{N_{xy_1} N_{yz_3}}{N_{yz_1}}\right]}{N_{xy_2} - \frac{N_{xy_1} N_{yz_2}}{N_{yz_1}}} .$$

Thus for any z, $(h_1(h_2(z),z),\ h_2(z),z)$ are the coordinates of a point on the Y axis. Using this 3-tuple, two points, G_1 and G_2, may arbitrarily be chosen on the Y axis:

$$G_1 = (h_1(h_2(0),0)\ ,\ h_2(0),0)$$

$$G_2 = (h_1(h_2(1),1)\ ,\ h_2(1),1) .$$

The equation of the Y axis in three space may then be written

$$\vec{Y} = G_1 + t\ (G_2 - G_1),$$

where t is a parameter.

The Y axis is perpendicular to the XZ plane. Thus any point S on the Y axis, such that the vector from F to S is perpendicular to the Y axis, lies in the XZ plane, making S the origin of the axis system. The perpendicularity requirement is satisfied if

$$(F-S) \cdot (G_2 - G_1) = 0 \quad , \qquad \text{(C.5)}$$

and since S is on the Y axis there is a particular value of the parameter t (say t_0) in the equation of the Y axis such that

$$S = G_1 + t_0(G_2-G_1). \tag{C.6}$$

Solving (C.5) and (C.6) simultaneously gives

$$t_0 = \frac{(F-G_1) \cdot (G_2-G_1)}{(G_2-G_1) \cdot (G_2-G_1)}$$

The final result needed to completely specify the anatomical axes system is

$$N_{xz} = N_{xy} \times N_{yz} \quad .$$

In application of this method one problem has been encountered. This occurs when the anatomical Z axis is perfectly aligned with the global Z axis (N_{xy} = (0, 0, 1)). In this situation the f, g, h_1, and h_2 functions all degenerate to $\frac{0}{0}$ situations. In order to avoid this problem, after N_{xy} has been computed it is checked to see if any of its components are greater than 0.99. If not, computation proceeds as normal. If there is such a component the coordinates of the defining landmarks are converted to an axis system which is a rotation of the global axis system, the rotation being 30 degrees about the vector (1, 1, 1). After this is performed computations are restarted and proceed as normal. When the resulting origin and direction cosines are obtained they are with respect to the rotated system, and thus in these cases, the reverse rotation must be applied to the results, giving the final results desired.

Referring to Table 4, it is obvious that not all anatomical axis systems are defined in exactly the same way as the one used in developing these equations. In fact there is a total of six different basic configurations, each of which is listed in Table 8. The equations developed, however, may be applied directly to anatomical axis system definition, by ignoring the names associated with the axes.

TABLE 8

ARRANGEMENT OF NORMAL VECTORS INTO THE DIRECTION COSINE MATRIX OF SEGMENT ANATOMICAL AXES WITH RESPECT TO GLOBAL AXES

CONFIGURATION OF ANATOMICAL AXIS SYSTEM DEFINITION		PLACEMENT OF NORMAL VECTORS INTO DIRECTION COSINE MATRIX		
XY	A, B, C	N_{XY}	$\rightarrow$	Row 3
YZ	D, E	N_{YZ}	$\rightarrow$	Row 1
XZ	F	N_{XZ}	$\rightarrow$	Row 2
XY	A, B, C	N_{XY}	$\rightarrow$	Row 3
XZ	D, E	N_{YZ}	$\rightarrow$	Row 2
YZ	F	N_{XZ}	$\rightarrow$	Row 1
YZ	A, B, C	N_{XY}	$\rightarrow$	Row 1
XY	D, E	N_{YZ}	$\rightarrow$	Row 3
XZ	F	N_{XZ}	$\rightarrow$	Row 2
YZ	A, B, C	N_{XY}	$\rightarrow$	Row 1
XZ	D, E	N_{YZ}	$\rightarrow$	Row 2
XY	F	N_{XZ}	$\rightarrow$	Row 3
XZ	A, B, C	N_{XY}	$\rightarrow$	Row 2
XY	D, E	N_{YZ}	$\rightarrow$	Row 3
YZ	F	N_{XZ}	$\rightarrow$	Row 1
XZ	A, B, C	N_{XY}	$\rightarrow$	Row 2
YZ	D, E	N_{YZ}	$\rightarrow$	Row 1
XY	F	N_{XZ}	$\rightarrow$	Row 3

The normal vectors resulting from the computations form the direction cosine matrix of that segment's anatomical axes with respect to global axes. It is here that the different configurations of the anatomical system definitions have their effect. Each normal vector becomes a row of the cosine matrix. The row the normal vector is placed in is determined by the particular anatomical axis system configuration (see Table 8).

APPENDIX D

DETERMINATION OF PRINCIPAL AXES

For each segment an inertial tensor is computed based on its volume distribution. The three eigenvalues of this tensor are the segment's principal moments of inertia. Associated with each eigenvalue is an eigenvector. These three vectors when normalized, are the rows of the direction cosine matrix of the principal axes with respect to the global axes, referred to as D_{PG}. The order that these vectors are placed in the direction cosine matrix is chosen so that the principal axis systems defined have the best possible alignment with the anatomical axes of the same segment.

Post multiplying D_{PG} by $(D_{AG})^T$, the transpose of the direction cosine matrix of the anatomical axis system of the same segment with respect to global axes, results in D_{PA}, the direction cosine matrix of the principal with respect to anatomical axes. The first diagonal element of D_{PA} is the cosine of the angle between the anatomical X vector and principal X vector. Similarly, the other two diagonal elements are the cosines of the angles between the anatomical and principal Y and Z vectors. Thus, if the largest element of each row of D_{PA} is on the diagonal, the eigenvectors have been placed into D_{PG} in proper order to align the two axis systems.

The method used to arrange eigenvectors into D_{PG}, is based on placing the eigenvectors into a matrix, A, in arbitrary order. The matrix product, $B = A\ (D_{AG})^T$ is computed. Rows of B are then interchanged so that, if possible, the largest element of each row is on the diagonal. The product relationship between B and A is maintained if identical row interchanges are performed on A. If it is possible to place the largest element of each row of B on the diagonal, the B and A matrices resulting from these interchanges are D_{PA} and D_{PG}, respectively. This is not always possible, though, since in a few cases, two rows of B will have their largest element in the same column. The following algorithm has been developed to handle all possible cases:

(1) The normalized eigenvectors are arranged as the rows of a matrix in arbitrary order. Call this matrix A.

(2) This matrix is post-multiplied by $(D_{AG})^T$. Call the product matrix B.

(3) The element of B with largest absolute value is determined. Let the position of this element be row i, column j.

(4) The j^{th} row of the matrix D_{PA} is filled from the i^{th} row of B. Likewise, the j^{th} row of D_{PG} is filled from the i^{th} row of A.

(5) Next, four positions of B are examined. These are the four elements of B not in row i and not in column j. Of these four values the one smallest in absolute value is chosen, say that its position is row k, column ℓ.

(6) Row k of B cannot be placed in row j of D_{PA} since this row is already filled, nor can it be placed in the ℓ^{th} row since this would give the worst possible alignment with the anatomical axes. Thus row k of B is placed in the only other row, row m. Likewise row k of A is placed in row m of D_{PG}. There is one row remaining unused in both A and B. These are placed in row ℓ of matrices D_{PG} and D_{PA}, respectively.

(7) D_{PA} is now examined to see if all diagonal elements are positive. For any diagonal elements that are negative, the entire row containing that diagonal element is multiplied by -1. The same row of D_{PG} is then also multiplied by -1.

D_{PG} which results from this process, is the direction cosine matrix of the segment principal axes with respect to the global axes. D_{PA}, which is also a result of this algorithm, is the direction cosine matrix of the segment principal axes with respect to the segment anatomical axes. The principal moments then take the name (i.e., X, Y, or Z) that their associated eigenvector has been assigned by this method.

APPENDIX E

PRODUCING TABLE OF (%) HEIGHT VERSUS (%) VOLUME

In the inertial analysis procedure a height is associated with each cross section. A volume is then computed to be associated with each cross section, as the volume of a right cylinder with this height and end surfaces identical to the cross section. If the Z coordinate of some cross section is Z_0, its assigned height h, and computed volume, v, the volume v is evenly distributed between $Z_0 + \frac{h}{2}$ and $Z_0 - \frac{h}{2}$.

In order to produce the table of height versus volume, the total height of a subject is divided into 200 intervals each of height Δh. A data storage location is associated with each of these height intervals. The storage locations are numbered from 1 to 200 and are initialized to zero. The volume associated with each cross section is then distributed between the storage locations associated with the same vertical interval as the cross section. The end result of this process is the measure of the total volume of a subject's body located vertically between $(i-1)\Delta h$ and $i\Delta h$ is stored in storage location i.

For the cross section mentioned, with Z coordinate Z_0 and height h, n is determined such that

$$(n-1)\ (\Delta h) < Z_0 - \frac{h}{2} < n\ (\Delta h)\ .$$

Then to storage location n,

$$\frac{n(\Delta h) - (Z_0 - \frac{h}{2})}{h} \cdot v$$

is added, where v is the volume associated with the cross section. Additionally a value m is determined such that

$$(m-1)\Delta h < Z_0 + \frac{h}{2} < m\ (\Delta h).$$

This time

$$\frac{z_0 + \frac{h}{2} - (m-1)\Delta h}{\Delta h} \cdot v$$

is added to storage location m. For each storage location between n and m, $\frac{h}{\Delta h} \cdot v$ is added. This process is repeated for each cross section.

The resulting storage locations contains the total amount of volume the subject's body has within each interval that is 1/2 percent of total height. The choice of 200 intervals was somewhat arbitrary, more intervals could have been used. This would have little effect upon end results, though, since spacing between cross sections is generally greater than 1 percent of total body height.

The values contained in the storage locations upon completion of this process can be used to produce a table of accumulated body volume up to specified points. This is done by summing the contents of all data storage locations corresponding to height intervals below those points.

APPENDIX F

SOURCE LISTING OF PROGRAMS SGMNTS, FLAPS, AND POLISH

```
C     PROGRAM SGMNTS*********************************************************
C
C
C     PROGRAM SGMNTS IS THE FIRST IN A SERIES OF THREE SEGMENTATION
C     ROUTINES, USED TO REGROUP BODY SURFACE DESCRIPTION DATA POINTS INTO
C     DATA POINTS DESCRIBING THE SURFACE OF 19 DIFFERENT BODY SEGMENTS.
C     SGMNTS RECEIVES DATA POINTS PRODUCED BY STEREOPHOTOMETRY AND GROUPED
C     INTO 5 SEGMENTS AND REGROUPS THIS DATA INTO A TOTAL OF 17 SEGMENTS.
C     THE REMAINING SEGMENTATION IS LEFT TO BE DONE BY THE OTHER SEGMEN-
C     TATION ROUTINES.
C
C     SGMNTS READS FROM TAPE7 THE BODY SURFACE DATA POINTS GROUPED INTO 5
C     SEGMENTS.  IT ALSO READS FROM INPUT THE NUMBERS TO BE ASSOCIATED
C     WITH THE DATA SETS THAT ARE SEGMENTED.  THIS INPUT IS IN THE FORM:
C     BEGINNING NUMBER, STOPPING NUMBER, AND INCREMENT.  THESE NUMBERS
C     ALSO DETERMINE HOW MANY DATA SETS WILL BE PROCESSED.  THE DATA
C     POINTS GROUPED INTO 17 SEGMENTS ARE WRITTEN OUT TO TAPES. THE
C     NUMBERS READ FROM INPUT ARE WRITTEN TO TAPE9 ALONG WITH THE NUMBER
C     OF CROSS SECTIONS PER EACH NEW SEGMENT.


C     COMMON AREAS
C
C.../PLANE/--DATA PERTAINING TO ONE OF THE ORIGINAL SEGMENTS WHICH IS
C       PRESENTLY BEING FURTHER SEGMENTED.
C     NORM--CONTAINS THE COMPONENTS OF THE NORMALS TO EACH SEGMENTING
C       PLANE.
C     IDEFPT--CONTAINS THE NUMBER OF THE LANDMARK USED TO DEFINE EACH SEG-
C       MENTING PLANE.
C     XYZLMK--COORDINATES OF EACH OF THE 76 ANTHROPOMETRIC LANDMARKS.
C     NCOL--NUMBER OF SEGMENTING PLANES.
C     LSTSG--LOGICAL VARIABLE EQUAL TO PROCESSING IS NOW BEING PERFORMED
C       ON THE LAST SEGMENT THE PRESENT SEGMENT IS TO BE DIVIDED INTO.
C
C.../POINTS/--DATA PERTAINING TO THE CROSS SECTION PRESENTLY BEING PRO-
C       CESSED.
C     X--X COORDINATES FOR ALL POINTS IN THE CROSS SECTION.
C     Y--Y COORDINATES FOR ALL POINTS IN THE CROSS SECTION.
C     NP--NUMBER OF DATA POINTS IN THE CROSS SECTION.
C     Z--COMMON Z COORDINATE OF ALL POINTS IN THE CROSS SECTION.
C
C.../STORER/--DATA PERTAINING TO THE STORAGE OF DATA POINTS PRODUCING
C       NEGATIVE DOT PRODUCTS AND SOME OTHER MISC. INFO.
C     ISTRPL--NUMBER OF CROSS SECTIONS STORED THUS FAR.
C     ISTORE--NUMBER OF DATA POINTS STORED FOR EACH OF THESE CROSS
C       SECTIONS.
C     XYSTOR--XY COORDINATES OF ALL STORED DATA POINTS.
C     ZSTOR--Z COORDINATES OF EACH CROSS SECTION WITH STORED DATA POINTS.
C     ISEGCT--CONTAINS THE NUMBER OF THE NEXT CROSS SECTION TO BE WRITTEN
C       OUT.
C     ITOTST--THE TOTAL NUMBER OF DATA POINTS STORED IN XYSTOR.
C     NSEGCS--ARRAY TO BE FILLED WITH THE NUMBER OF CROSSECTIONS PER EACH
C       NEW SEGMENT.
C     ISEG--THE NUMBER OF THE NEW SEGMENT WHICH DATA IS PRESENTLY BEING
C       WRITTEN OUT FOR.
C
C.../PLACE/--DATA PERTAINING TO THE DOT PRODUCTS COMPUTED.
C     ICOL--SPECIFIES WHICH COLUMN OF PDOT IS PRESENTLY BEING USED.
```

```
C   PDOT--THE DOT PRODUCT FOR EACH DATA POINT IN THE PRESENT CROSS SEC-
C     TION WITH EACH SEGMENTING PLANE OF THE PRESENT SEGMENT.
C
C        '
C*************************************************************************
      PROGRAM SGMNTS (INPUT,OUTPUT,TAPE7,TAPE5,TAPE9,TAPE3=INPUT)
      LOGICAL LSTSG, DBLCUT
      REAL NORM
      COMMON /PLANE/ NORM(3,6),IDEFPT(6),XYZLMK(76,3),NCOL,LSTSG
      COMMON /POINTS/ X(99),Y(99),NP,Z
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,150),ZSTOR(20),ISEGCT,
     &ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL,PDOT(99,6)
      INTEGER NPLNS(5)

C   NUMBERS OF THE DATA SETS TO BE PROCESSED ARE READ IN.
      READ (3,11) ISTRT,ISTP,INC
      WRITE (9,11) ISTRT,ISTP,INC
      DO 1000 ISUB=ISTRT,ISTP,INC
      ISEG = 0
      DO 900 I=1,21
900   NSEGCS(I) = 0
      DO 7  I=1,16
      READ(7,99)
7     CONTINUE

C   NUMBER OF CROSS SECTIONS PER ORIGINAL SEGMENT IS READ IN.
      READ (7,77) NPLNS
      CALL ZCORS (NPLNS)
      DO 88 I=1,3
      READ (7,77)
88    CONTINUE

      DO 100 ISECT =1,5
      GOTO (120,140,160,180,200),ISECT
120   CALL HDTRUNK
      DBLCUT = .TRUE.
      GOTO 250
140   CALL RTARM
      DBLCUT = .FALSE.
      GOTO 250
160   CALL LTARM
      GOTO 250
180   CALL RTLEG
      GOTO 250
200   CALL LTLEG
250      NPL = NPLNS(ISECT)
         ITOTST = ISEGCT = ISTRPL = 0
         ICOL = 1
         LSTSG = .FALSE.
C
C   EACH CROSS SECTION WITHIN ORIGINAL SEGMENT ISECT IS PROCESSED.
         DO 300 IPLANE = 1,NPL
            READ (7,9) NP,Z
            IF (NP.GE.100) STOP "X, Y, AND PDOT UNDER DIMENSIONED IN SGM
     &NTS"
            READ (7,10) (X(L),Y(L),L=1,NP)
            CALL DOT
            IF (DBLCUT) CALL COMPRS
            CALL SORT
300         IF (DBLCUT) NCOL = NCOL +2
         ISEG = ISEG +1
```

```
         NSEGCS(ISEG) = ISEGCT
100      CONTINUE
         WRITE(9,99) NSEGCS
         READ (7,99)
         IF (EOF(7).EQ.0) STOP "END OF FILE NOT FOUND"
1000     CONTINUE

         ENDFILE 5
         ENDFILE 9
         STOP  "FROM SGMNTS"
9        FORMAT(5X,I4,10X,F6.2)
10       FORMAT(1X,12F6.2)
11       FORMAT (3I5)
77       FORMAT (1X,5I10)
99       FORMAT (4X,21I3)
         END



C     SUBROUTINE DOT COMPUTES DOT PRODUCTS FOR EACH DATA POINT IN THE
C        PRESENT CROSS SECTION.
C
C
         SUBROUTINE DOT
         REAL NORM
         COMMON /PLANE/ NORM(3,6),IDEFPT(6),XP(76),YP(76),ZP(76),NCOL
         COMMON /POINTS/ X(99),Y(99),NP,Z
         COMMON /PLACE/ DUM,PDOT(99,6)
         DO 100 J=1,NCOL
         PZ = Z - ZP(IDEFPT(J))
         DO 100 I=1,NP
100      PDOT(I,J) = NORM(1,J)*(X(I) - XP(IDEFPT(J)))
     &               +NORM(2,J)*(Y(I) - YP(IDEFPT(J)))
     &               +NORM(3,J)*PZ
         RETURN
         END
```

```
*   SUBROUTINE HDTRUNK DEFINES PLANES SEPARATING THE HEAD TRUNK SEGMENT
C     INTO HEAD, NECK, THORAX, ABDOMEN, AND PELVIS.
C
C
      SUBROUTINE HDTRUNK
      IMPLICIT REAL (N)
      INTEGER NCOL
      COMMON /PLANE/ N1X,N1Y,N1Z,N2DX,N2DY,N2DZ,N3X,N3Y,N3Z,N4X,N4Y,N4Z
     &,N2HX,N2HY,N2HZ,N2H2X,N2H2Y,N2H2Z,IDEFPT(6),XP(76),YP(76),ZP(76),
     & NCOL

      NCOL = 6
      IDEFPT(1) = 39
      IDEFPT(2) = 43
      IDEFPT(3) = 7
      IDEFPT(4) = 52
      IDEFPT(5) = 2
      IDEFPT(6) = 43

*     HEAD - VECTOR FROM LEFT GONION TO RIGHT GONION
      RA1X= XP(48) - XP(39)
      RA1Y= YP(48) - YP(39)
      RA1Z= ZP(48) - ZP(39)
*     HEAD - VECTOR FROM LEFT GONION TO NUCHALE
      RB1X= XP(1) - XP(39)
      RB1Y= YP(1) - YP(39)
      RB1Z= ZP(1) - ZP(39)
*     NORMAL TO HEAD PLANE
      N1X= (RB1Y * RA1Z) - (RB1Z * RA1Y)
      N1Y= -((RB1X * RA1Z) - (RB1Z * RA1X))
      N1Z= (RB1X * RA1Y) - (RB1Y * RA1X)
*     NORMAL TO NECK HORIZONTAL PLANE
      N2HX = N2H2X = 0.
      N2HY = N2H2Y = 0.
      N2HZ = N2H2Z = 1.
*     NORMAL TO NECK DIAGONAL PLANE
      N2DX= 0
      N2DY= 1
      N2DZ= 1
*     NORMAL TO THORAX HORIZONTAL PLANE
      N3X= 0
      N3Y= 0
      N3Z= 1
*     NORMAL TO ABDOMINAL HORIZONTAL PLANE
      N4X= 0
      N4Y= 0
      N4Z= 1

      RETURN
      END
```

```
*     SUBROUTINE RTARM DEFINES SEGMENTING PLANES SEPARATING THE RIGHT ARM
C       INTO AN UPPER ARM, LOWER ARM, AND HAND.
C
C
        SUBROUTINE RTARM
        IMPLICIT REAL (N)
        INTEGER NCOL
        COMMON /PLANE/ NORM(3,6),IDEFPT(6),XP(76),YP(76),ZP(76),NCOL
        EQUIVALENCE (NORM(1,1),N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z),(NORM(
       &1,2),N2X),(NORM(2,2),N2Y),(NORM(3,2),N2Z)

        NCOL = 2
        IDEFPT (1) = 14
        IDEFPT (2) = 22

*       RT ELBOW PLANE
*       VECTOR FROM RT LATERAL HUMERAL EPICON
*       (PT 12) TO RT OLECRANON (PT 14)
        RAX= XP(14) - XP(12)
        RAY= YP(14) - YP(12)
        RAZ= ZP(14) - ZP(12)
*       VECTOR FROM RT LATERAL HUMERAL EPICON (PT 12)
*       TO RT MEDIAL HUMERAL EPICON (PT 18)
        RBX= XP(18) - XP(12)
        RBY= YP(18) - YP(12)
        RBZ= ZP(18) - ZP(12)
*       NORMAL VECTOR TO PLANE CONTAINING RA AND RB
*       VECTORS (RT ELBOW PLANE)
        N1X= (RBY*RAZ)- (RBZ*RAY)
        N1Y= -((RBX*RAZ)- (RBZ*RAX))
        N1Z= (RBX*RAY)- (RBY*RAX)
*       RT WRIST PLANE
*       NORMAL TO RT WRIST PLANE
        N2X= 0
        N2Y= YP(16) - YP(20)
        N2Z= ZP(16) - ZP(20)

        RETURN
        END
```

```
*    SUBROUTINE LTARM DEFINES SEGMENTING PLANES SEPARATING THE LEFT ARM
C      INTO UPPER ARM, LOWER ARM, AND HAND.
C
C
       SUBROUTINE LTARM
       IMPLICIT REAL (N)
       INTEGER NCOL
       COMMON /PLANE/ NORM(3,6),IDEFPT(6),XP(76),YP(76),ZP(76),NCOL
       EQUIVALENCE (NORM(1,1),N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z),(NORM(
     &1,2),N2X),(NORM(2,2),N2Y),(NORM(3,2),N2Z)

       NCOL = 2
*      LT ELBOW PLANE
*      VECTOR FROM LT OLECRANON(PT13) TO LT
*      LATERAL HUMERAL EPICON(PT11)
       RAX= XP(11) - XP(13)
       RAY= YP(11) - YP(13)
       RAZ= ZP(11) - ZP(13)
*      VECTOR FROM LT OLECRANON(PT13) TO LT MEDIAL
*      HUMERAL EPICON(PT9)
       RBX= XP(9) - XP(13)
       RBY= YP(9) - YP(13)
       RBZ= ZP(9) - ZP(13)
*      NORMAL VECTOR TO PLANE CONTAINING RA AND RB
*      VECTORS (LT ELBOW PLANE)
       N1X= (RBY*RAZ)- (RBZ*RAY)
       N1Y= -((RBX*RAZ)- (RBZ*RAX))
       N1Z= (RBX*RAY)- (RBY*RAX)
*      LT WRIST PLANE
*      NORMAL TO LT WRIST PLANE
       N2X= 0
       N2Y= YP(15) - YP(19)
       N2Z= ZP(15) - ZP(19)

       IDEFPT (1) = 13
       IDEFPT(2) = 21
       RETURN
       END
```

```
*    SUBROUTINE RTLEG DEFINES SEGMENTING PLANES SEPARATING THE RIGHT LEG
C      INTO UPPER LEG, CALF, AND FOOT.
C
C
       SUBROUTINE RTLEG
       IMPLICIT REAL (N)
       INTEGER NCOL
       COMMON /PLANE/ NORM(3,6),IDEFPT(6),XYZLMK(76,3),NCOL
       EQUIVALENCE (NORM(1,1),N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z),(NORM(
     &1,2),N2X),(NORM(2,2),N2Y),(NORM(3,2),N2Z)

       NCOL = 2
       IDEFPT(1) = 59
       IDEFPT(2) = 69

*      NORMAL TO RIGHT KNEE PLANE

       N1X= 0
       N1Y= 0
       N1Z= 1

*      NORMAL TO RT ANKLE PLANE

       N2X= 0
       N2Y= 0
       N2Z= 1


       RETURN
       END
```

```
*    SUBROUTINE LTLEG DEFINES SEGMENTING PLANES SEPARATING THE LEFT LEG
C      INTO UPPER LEG, CALF, AND FOOT.
C
C
       SUBROUTINE LTLEG
       IMPLICIT REAL (N)
       INTEGER NCOL
       COMMON /PLANE/ NORM(3,6),IDEFPT(6),XYZLMK(76,3),NCOL
       EQUIVALENCE (NORM(1,1),N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z),(NORM(
      &1,2),N2X),(NORM(2,2),N2Y),(NORM(3,2),N2Z)

       NCOL = 2
       IDEFPT(1) = 58
       IDEFPT(2) = 68

*      NORMAL TO LEFT KNEE PLANE

       N1X= 0
       N1Y= 0
       N1Z= 1


*      NORMAL TO LEFT ANKLE PLANE

       N2X= 0
       N2Y= 0
       N2Z= 1


       RETURN
       END
```

```
*    SUBROUTINE ZCORS READS IN THE Z COORDINATES OF ALL CROSS SECTIONS AS
C      LISTED AT THE BEGINNING OF THE DATA.  USING THESE, ZCORS DETER-
C      MINES TWO Z COORDINATES.  ONE, THE AVERAGE OF THE Z COORDINATE OF
C      THE FIRST CROSS SECTION OF THE LEFT UPPER ARM AND THE Z COORDINATE
C      OF THE CROSS SECTION IN THE THORAX IMMEDIATELY ABOVE THIS.  THE
C      OTHER Z COORINATE IS COMPUTED SIMILARILY USING THE RIGHT ARM.
C      THESE TWO Z COORDINATES ARE WRITTEN OUT AS A 77TH AND 78TH
C      LANDMARK.
C
C
       SUBROUTINE ZCORS (NPLNS)
       COMMON /POINTS/  Z(100)
       INTEGER NPLNS(5)
       REAL ZCOR(2)
       ISKIP(II) = (II + 11)/12

       ISTP = NPLNS(1)
       READ (7,99) (Z(I),I=1,ISTP)
       READ (7,99) ZCOR(1)
       ISTP = ISKIP(NPLNS(2)) -1
       DO 10 I=1,ISTP
10     READ (7,99)
       READ (7,99) ZCOR(2)
       ISTP = ISKIP(NPLNS(3)) + ISKIP(NPLNS(4)) + ISKIP(NPLNS(5)) -1
       DO 20 I=1,ISTP
20     READ (7,99)
       DO 40 II=1,2
       I = 0
30     I = I +1
       IF (Z(I).GT.ZCOR(II)) GOTO 30
40     ZCOR(II) = (Z(I-1) + ZCOR(II))/2.
       CALL LANDMK
       WRITE (5,88) ZCOR
       RETURN
88     FORMAT (25X,F10.2)
99     FORMAT (1X,12F6.2)
       END
```

```
*    SUBROUTINE LANDMK READS IN THE 76 ANTHROPOMETRIC LANDMARKS IN THE
C      DATA SET.  IT ALSO DETERMINES IF THE ACTUAL COORDINATES OF THE
C      LANDMARK NEED TO BE COMPUTED.
C
C
       SUBROUTINE LANDMK
       COMMON /PLANE/ DUM(24),XYZLMK(76,3)
       REAL PROX(3),DIS(3)
       DO 100 I=1,76
       READ (7,99) PROX,DIS
C
C    IF DIS = (0,0,0) THEN THE COORDINATES OF THE LANDMARK ARE IDENT-
C      ICALLY THOSE OF PROX; ELSE COMB IS CALLED TO COMPUTE THE COORDI-
C      NATES OF THE LANDMARK.
       DO 200 J=1,3
       IF (DIS(J).EQ.0) GOTO 200
       CALL COMB (PROX,DIS)
       GOTO 75
200    CONTINUE
75     DO 100 J=1,3
100    XYZLMK(I,J) = PROX(J)
       WRITE (5,88) (I,(XYZLMK(I,J),J=1,3),I=1,76)
       RETURN
88     FORMAT (I5,3F10.2)
99     FORMAT (5X,3F10.2,3X,3F10.2)
       END



C    SUBROUTINE COMB IS USED TO COMPUTE THE ACTUAL LOCATION OF AN ANTHRO-
C      POMETRIC LANDMARK.  THIS LOCATION IS ON THE LINE BETWEEN THE
C      POINTS PROX AND DIS, 3/4 INCH FROM PROX IN THE DIRECTION OF DIS.
C
C
       SUBROUTINE COMB  (PROX,DIS)
       REAL PROX(3),DIS(3),XYZ(3),LENGTH
       LENGTH = 0.
       DO 100 I=1,3
       XYZ(I) = DIS(I) - PROX(I)
100    LENGTH = LENGTH + XYZ(I)**2
       LENGTH = .75  *2.54/SQRT(LENGTH)
       DO 200 I=1,3
       XYZ(I) = LENGTH*XYZ(I)
200    PROX(I) = PROX(I) + XYZ(I)
       RETURN
       END
```

```
*    SUBROUTINE SORT CONTROLS PROCESSING OF EACH CROSS SECTION.
C
C
      SUBROUTINE SORT
      LOGICAL LSTSG
      COMMON /PLANE/ NORM(3,6),IDEFPT(6),XY2P(228),NCOL,LSTSG
      COMMON /POINTS/ X(99),Y(99),NPTS,Z
      COMMON /STORER/ ISTRPL,ISTORE(28),XYSTOR(2,150),ZSTOR(28),ISEGCT
     &,ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL,PDOT(99,6)

      CALL LOOK  (COLSG)
      IF  (COLSG) 300,200,100

300   IF (LSTSG) GOTO 100
      LSTSG = ICOL.GE.NCOL
      CALL UNSTOR

100   ISEGCT = ISEGCT +1
      WRITE (5,88) ISEGCT,NPTS,Z
      WRITE (5,99) (X(I),Y(I), I=1,NPTS)
      RETURN

200   CALL SEP
      RETURN

88    FORMAT (1X,2I4,8X,F8.2)
99    FORMAT (1X,12F6.2)
      END



C    SUBROUTINE LOOK EXAMINES THE COLUMN OF DOT PRODUCTS FOR A CROSS
C      SECTION. IF ALL DOT PRODUCTS ARE POSITIVE COLSG IS RETURNED WITH A
C      POSITIVE VALUE.  IF ALL ARE NEGATIVE COLSG IS RETURNED WITH A
C      NEGATIVE VALUE.  IF THE DOT PRODUCTS ARE OF MIXED SIGN COLSG IS
C      RETURNED AS 0. DOT PRODUCTS OF VALUE 0 ARE IGNORED IN THIS EXAM-
C      INATION.
C
C
      SUBROUTINE LOOK  (COLSG)
      COMMON /POINTS/ DUM(198),NPTS
      COMMON /PLACE/ ICOL,PDOT(99,6)
      ISTRT = 0
10    ISTRT = ISTRT +1
      IF (ISTRT.GE.NPTS) GOTO 150
      IF (PDOT(ISTRT,ICOL).EQ.0.) GOTO 10

      COLSG = PDOT (ISTRT,ICOL)
      ISTRT = ISTRT +1
      DO 100 I=ISTRT,NPTS
      IF (PDOT(I,ICOL)*COLSG .GE. 0.) GOTO 100
      COLSG = 0.
      RETURN
100   CONTINUE
      RETURN

150   COLSG = PDOT(ISTRT,ICOL)
      IF (COLSG.EQ.0.)  COLSG = 1.
      RETURN
      END
```

```
*    SUBROUTINE SEP IS CALLED FOR A CROSS SECTION WHICH HAS DOT PRODUCTS
C      OF MIXED SIGNS.  IT CONTROLS THE STORAGE OF DATA POINTS YIELDING
C      NEGATIVE DOT PRODUCTS, THE WRITING OF DATA POINTS WITH POSITIVE
C      DOT PRODUCTS, AND THE CREATION OF TWO NEW DATA POINTS.
C
C
      SUBROUTINE SEP
      REAL XYTEMP (2,99)
      LOGICAL SNGLPT
      COMMON /POINTS/ X(99),Y(99),NPTS,Z
      COMMON /PLACE/ ICOL,PDOT(99,6)
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR ( 300),ZSTOR(20),ISEGCT

      ITEMP = 0
      ISTRPL = ISTRPL +1
      IF (ISTRPL.GT.20) STOP "ISTOR AND ZSTOR UNDER DIMENSIONED IN SGNMT
     &S"
      ZSTOR (ISTRPL) = Z
      ISTORE(ISTRPL) = 0
      SNGLPT = .FALSE.
      SIGN = PDOT (1,ICOL)

      DO 100 I=1,NPTS
         IF (SIGN*PDOT(I,ICOL).GT.0) GOTO 50
         CALL ADDPT (I,ITEMP,XYTEMP)
         SIGN = PDOT(I,ICOL)
         SNGLPT = .NOT.SNGLPT
50    IF (PDOT(I,ICOL).LT.0) GOTO 75
         CALL TEMPST (X(I), Y(I), ITEMP, XYTEMP)
         GOTO 100
75    CALL STORE (X(I),Y(I))
100   CONTINUE

      IF (SNGLPT) CALL ADDPT (1,ITEMP,XYTEMP)
      ISEGCT = ISEGCT +1
      WRITE (5,88) ISEGCT,ITEMP,Z
      WRITE (5,99) ((XYTEMP(I,J),I=1,2),J=1,ITEMP)

      RETURN
88    FORMAT (1X,2I4,8X,F8.2)
99    FORMAT (1X,12F6.2)
      END
```

```
*     SUBROUTINE ADDPT COMPUTES THE COORDINATES OF ONE OF THE PAIR OF
C       POINTS TO BE ADDED TO A CROSS SECTION WITH DOT PRODUCTS OF MIXED
C       SIGNS.
C
C
      SUBROUTINE ADDPT (I,ITEMP,XYTEMP)
      IMPLICIT REAL (N)
      REAL XYTEMP (198)
      INTEGER NPTS
      COMMON /POINTS/ X(99),Y(99),NPTS,Z
      COMMON /PLANE/ NORM(3,6),IDEFPT(6),XP(76),YP(76),ZP(76)
      COMMON /PLACE/ ICOL
      C1 = X(I)
      C2 = Y(I)
      IF (I.EQ.1) GOTO 25
      B1 = X(I-1)
      B2 = Y(I-1)
      GOTO 50
25    B1 = X(NPTS)
      B2 = Y(NPTS)
50    N1 = NORM (1,ICOL)
      N2 = NORM (2,ICOL)
      N3 = NORM (3,ICOL)
      A1 = XP(IDEFPT(ICOL))
      A2 = YP(IDEFPT(ICOL))
      A3 = ZP(IDEFPT(ICOL))
      IF (B1.EQ.C1) GOTO 100
      SLOPE = (B2-C2)/(B1-C1)
      XADD = (N3*(A3 - Z) + N1*A1 + N2*(SLOPE*B1 + A2 - B2))
      XADD = XADD/(N1 + N2*SLOPE)
      YADD = SLOPE*(XADD - B1) + B2
      GOTO 150
100   XADD = B1
      YADD = (N1*(A1-B1) + N3*(A3-Z))/N2 + A2
150   CALL TEMPST (XADD,YADD,ITEMP,XYTEMP)
      CALL STORE (XADD,YADD)
      RETURN
      END
```

```
*     SUBROUTINE STORE STORES POINTS WITH NEGATIVE DOT PRODUCTS FROM A
C       CROSS SECTION HAVING DOT PRODUCTS OF BOTH SIGN.
C
C
        SUBROUTINE STORE (X,Y)
        COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,150),DUM(21),ITOTST
        ITOTST = ITOTST +1
        IF (ITOTST.GT.150) STOP "XYSTOR UNDER DIMENSIONED IN SGMST2"
        XYSTOR (1,ITOTST) = X
        XYSTOR (2,ITOTST) = Y
        ISTORE(ISTRPL) = ISTORE(ISTRPL) +1
        RETURN
        END


C     SUBROUTINE TEMPST STORES DATA POINTS YIELDING POSITIVE DOT PRODUCTS
C       FROM A CROSS SECTION WITH DOT PRODUCTS OF MIXED SIGNS.  THESE
C       POINTS ARE STORED ONLY UNTIL THIS CROSS SECTION HAS BEEN COM-
C       PLETELY PROCESSED.
C
C
        SUBROUTINE TEMPST (X,Y,ITEMP,XYTEMP)
        REAL XYTEMP (2,99)
        IF (ITEMP.GE.100) STOP "XYTEMP UNDER DIMENSIONED IN SGMNTS"
        ITEMP = ITEMP +1
        XYTEMP (1,ITEMP) = X
        XYTEMP (2,ITEMP) = Y
        RETURN
        END
```

```
*   SUBROUTINE UNSTOR IS CALLED WHEN A CROSS SECTION WITH ALL NEGATIVE
C     DOT PRODUCTS IS ENCOUNTERED.  IF DATA POINTS HAVE BEEN STORED THEY
C     ARE WRITTEN OUT BY UNSTOR.  ALSO VARIOUS COUNTERS ARE RESET.
C
C
      SUBROUTINE UNSTOR
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,150),ZSTOR(20),ISEGCT,
     &ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL

      ISEG = ISEG +1
      NSEGCS(ISEG) = ISEGCT
      ISEGCT = 0
      ISTRT = 1
      ISTP = 0

100   IF (ISEGCT.GE.ISTRPL) GOTO 200
      ISEGCT = ISEGCT +1
      ISTR = ISTORE (ISEGCT)
      WRITE (5,88) ISEGCT,ISTR,ZSTOR (ISEGCT)
      ISTP = ISTP +ISTR
      WRITE (5,99) ((XYSTOR(I,J),I=1,2),J=ISTRT,ISTP)
      ISTRT = ISTP +1
      GOTO 100

200   ISTRPL = ITOTST = 0
      ICOL = ICOL +1

      RETURN
88    FORMAT (1X,2I4,8X,F8.2)
99    FORMAT (1X,12F6.2)
      END



C   SUBROUTINE COMPRS IS CALLED TO ASSIGN ONE DOT PRODUCT TO EACH DATA
C     POINT BEING SEPARATED BETWEEN THE NECK AND THORAX.  THREE SEGMEN-
C     TATION PLANES ARE USED FOR THIS SEPARATATION, THUS THREE DOT PRO-
C     DUCTS ARE COMPUTED, WHICH MUST BE COMBINED INTO ONE.
C
C
      SUBROUTINE COMPRS
      COMMON /PLACE/ ICOL,PDOT(99,6)
      COMMON /POINTS/ DUM1(198),NPTS
      COMMON /PLANE/ DUM2(252),NCOL
      NCOL = NCOL -2
      DO 100 I=1,NPTS
      IF (PDOT(I,5).GT.0.) GOTO 75
      IF (PDOT(I,2).GT.0. .AND. PDOT(I,6).GT.0.) GOTO 75
      PDOT(I,2) = -1
      GOTO 100
75    PDOT (I,2) = 1
100   CONTINUE
      RETURN
      END
```

```
C     PROGRAM FLAPS*************************************************************
C
C
C     PROGRAM FLAPS IS THE SECOND IN A SERIES OF THREE SEGMENTATION
C     ROUTINES, USED TO REGROUP BODY SURFACE DESCRIPTION DATA POINTS INTO
C     DATA POINTS DESCRIBING THE SURFACE OF 19 DIFFERENT BODY SEGMENTS.
C     FLAPS RECEIVES THE DATA OUTPUT BY SGMNTS AND SEPARATES THE LEFT
C     SHOULDER FLAP FROM THE THORAX SEGMENT AND SEPARATES THE LEFT HIP
C     FLAP FROM THE PELVIS SEGMENT.  FLAPS IS THEN RAN A SECOND TIME,
C     REPROCESSING THE OUTPUT FROM ITS PREVIOUS RUN.  THIS TIME IT SEPAR-
C     ATES THE RIGHT SHOULDER FLAP FROM THE THORAX AND THE RIGHT HIP FLAP
C     FROM THE PELVIS.
C
C     FLAPS READS BODY SURFACE DESCRIPTION DATA POINTS FROM TAPE7.  IT
C     ALSO READS THE NUMBERS OF THE DATA SETS TO BE PROCESSED FROM TAPE3,
C     ALONG WITH THE NUMBER OF CROSS SECTION PER SEGMENT OF THE READ IN
C     DATA.  THE DATA POINTS RESULTING FROM THE PROCESSING OF FLAPS ARE
C     WRITTEN TO TAPE5, AND THE DATA SETS PROCESSED AND RESULTING NUMBER
C     OF CROSS SECTIONS PER EACH SEGMENT IS WRITTEN TO TAPE9.


C     COMMON AREAS
C
C.../PLANE/--DATA PERTAINING TO ONE OF THE SEGMENTS OF THE READ IN DATA,
C       WHICH IS PRESENTLY BEING FURTHER SEGMENTED.
C     NORM--CONTAINS THE COMPONENTS OF THE NORMALS TO EACH SEGMENTING
C       PLANE.
C     IDEFPT--CONTAINS THE NUMBER OF THE LANDMARK USED TO DEFINE EACH SEG-
C       MENTING PLANE.
C     XYZLMK--COORDINATES OF EACH OF THE 76 ANTHROPOMETRIC LANDMARKS.
C     NCOL--NUMBER OF SEGMENTING PLANES.
C
C.../POINTS/--DATA PERTAINING TO THE CROSS SECTION PRESENTLY BEING PRO-
C       CESSED.
C     X--X COORDINATES FOR ALL POINTS IN THE CROSS SECTION.
C     Y--Y COORDINATES FOR ALL POINTS IN THE CROSS SECTION.
C     NP--NUMBER OF DATA POINTS IN THE CROSS SECTION.
C     Z--COMMON Z COORDINATE OF ALL POINTS IN THE CROSS SECTION.
C
C.../STORER/--DATA PERTAINING TO THE STORAGE OF DATA POINTS PRODUCING
C       NEGATIVE DOT PRODUCTS AND SOME OTHER MISC. INFO.
C     ISTRPL--NUMBER OF CROSS SECTIONS STORED THUS FAR.
C     ISTORE--NUMBER OF DATA POINTS STORED FOR EACH OF THESE CROSS
C       SECTIONS.
C     XYSTOR--XY COORDINATES OF ALL STORED DATA POINTS.
C     ZSTOR--Z COORDINATES OF EACH CROSS SECTION WITH STORED DATA POINTS.
C     ISEGCT--CONTAINS THE NUMBER OF THE NEXT CROSS SECTION TO BE WRITTEN
C       OUT.
C     ITOTST--THE TOTAL NUMBER OF DATA POINTS STORED IN XYSTOR.
C     NSEGCS--ARRAY TO BE FILLED WITH THE NUMBER OF CROSSECTIONS PER EACH
C       NEW SEGMENT.
C     ISEG--THE NUMBER OF THE NEW SEGMENT WHICH DATA IS PRESENTLY BEING
C       WRITTEN OUT FOR.
C
C.../PLACE/--DATA PERTAINING TO THE DOT PRODUCTS COMPUTED.
C     ICOL--SPECIFIES WHICH COLUMN OF PDOT IS PRESENTLY BEING USED.
C     PDOT--THE DOT PRODUCT FOR EACH DATA POINT IN THE PRESENT CROSS SEC-
C       TION WITH EACH SEGMENTING PLANE OF THE PRESENT SEGMENT.
```

```
C    NPNLS--NUMBER OF CROSS SECTIONS PER SEGMENT OF DATA READ IN.
C    ISECT--NUMBER OF THE SEGMENT BEING PROCESSED.
C
C
C***************************************************************************
      PROGRAM FLAPS (INPUT,OUTPUT,TAPE5,TAPE7,TAPE3,TAPE9)
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XYZLMK(70,3),LSTSG
      COMMON /POINTS/ X(99),Y(99),NP,Z
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,250),ZSTOR(20),ISEGCT,
     &ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL,PDOT(99,5),NPNLS(21),ISECT
      EXTERNAL SORT,SORT2
      LOGICAL LEFT

C    NUMBERS OF THE DATA SETS TO BE PROCESSED ARE READ IN.
      READ (3,11) ISTRT,ISTP,INC
      WRITE (9,11) ISTRT,ISTP,INC
      DO 1000 ISUB=ISTRT,ISTP,INC
      ISEG = ISECT = 0
      DO 900 I=1,25
900   NSEGCS(I) = 0

C    NUMBER OF CROSS SECTIONS PER EACH EXISTING SEGMENT IS READ IN.
      READ (3,99) NPNLS
C    IF NPNLS(18) AND NPNLS(19) BOTH EQUAL 0 THEN FLAPS ON THE LEFT SIDE
C     OF THE BODY ARE REMOVED, ELSE FLAPS ON THE RIGHT SIDE OF THE BODY
C     ARE REMOVED.
      LEFT = NPNLS(18) + NPNLS(19)  .EQ.  0

      DO 10 I=1,70
      READ(7,88) II,(XYZLMK( I,J),J=1,3)
10    WRITE(5,88) II,(XYZLMK( I,J),J=1,3)
      CALL SKIP (2)
      IF (LEFT) GOTO25
      ISKIP = 2
      CALL RSHFLP
      GOTO 50
25    ISKIP = 1
      CALL LSHFLP
50    CALL SGMNT (SORT2)
      CALL SKIP (ISKIP)
      IF (LEFT) GOTO 75
      CALL RHPFLP
      GOTO 100
75    CALL LHPFLP
100   CALL SGMNT (SORT)
      CALL SKIP (ISKIP+11)
      WRITE(9,99) NSEGCS
1000  CONTINUE

      ENDFILE 3
      ENDFILE 5
      STOP "FROM FLAPS"
11    FORMAT (3I5)
88    FORMAT (I5,3F10.2)
99    FORMAT (4X,21I3)
      END
```

```
*    SUBROUTINE SGMNTS READS IN EACH CROSS SECTION AND CONTROLS THE EXAM-
C      INATION OF DATA POINTS WITHIN THE CROSS SECTION.
C
C
      SUBROUTINE SGMNT (SORTER)
      LOGICAL LSTSG
      COMMON /POINTS/ X(99),Y(99),NP,Z
      COMMON /STORER/ ISTRPL,DUM(540),ISEGCT,ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL,PDOT(99,5),NPNLS(21),ISECT
      COMMON /PLANE/ DUM1(254),LSTSG
      ISECT = ISECT +1
         NPL = NPNLS(ISECT)
         ITOTST = ISEGCT = ISTRPL = 0
         LSTSG = .FALSE.
         DO 300 IPLANE = 1,NPL
            READ (7,9) NP,Z
            READ (7,10) (X(L),Y(L),L=1,NP)
            CALL DOT
            IF (ICOL.GT.1) CALL COMPRS
300         CALL SORTER
      IF (ISTRPL.GT.0) CALL UNSTOR
         ISEG = ISEG +1
         NSEGCS(ISEG) = ISEGCT
      RETURN
9     FORMAT (5X,I4,10X,F5.2)
10    FORMAT (1X,12F6.2)
      END
```

```
*    SUBROUTINE DOT COMPUTES DOT PRODUCTS FOR EACH DATA POINT IN THE
C      PRESENT CROSS SECTION.
C
C
      SUBROUTINE DOT
      REAL NORM
      COMMON /POINTS/ X(99),Y(99),NP,Z
      COMMON /PLACE/ ICOL,PDOT(99,5)
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XP(78),YP(78),ZP(78)
      DO 100 J=1,ICOL
      PZ = Z - ZP(IDEFPT(J))
      DO 100 I=1,NP
100   PDOT(I,J) = NORM(1,J)*(X(I) - XP(IDEFPT(J)))
     &            +NORM(2,J)*(Y(I) - YP(IDEFPT(J)))
     &            +NORM(3,J)*PZ
      RETURN
      END



C    SUBROUTINE SKIP IS USED TO SKIP OVER NSEG SEGMENTS WHICH REQUIRE
C      NO PROCESSING.
C
C
      SUBROUTINE  SKIP (NSEG)
      COMMON /POINTS/ X(99),Y(99),NPTS,Z
      COMMON /PLACE/ DUM(496),NPLNS(21),ISECT
      COMMON /STORER/ DUM2(543),NSEGCS(21),ISEG
      DO 100 I=1,NSEG
      ISECT = ISECT +1
      ISEG = ISEG +1
      NPL = NPLNS(ISECT)
      NSEGCS(ISEG) = NPL
      DO 100 J=1,NPL
      READ (7,99) IPLANE,NPTS,Z
      WRITE (5,99) IPLANE,NPTS,Z
      READ(7,88) (X(L),Y(L),L=1,NPTS)
      WRITE(5,88) (X(L),Y(L),L=1,NPTS)
100   CONTINUE
      RETURN
88    FORMAT (1X,12A6)
99    FORMAT (1X 2I4,8X,A8)
      END
```

```
*    SUBROUTINE RSHFLP DEFINES  SEGMENTING PLANES SEPARATING THE RIGHT
C      SHOULDER FLAP FROM THE THORAX.
C
C
      SUBROUTINE RSHFLP
      IMPLICIT REAL (N)
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XP(78),YP(78),ZP(78)
      COMMON /PLACE/ ICOL
      EQUIVALENCE (NORM,N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z)
      EQUIVALENCE (N2X,NORM(1,2)),(N2Y,NORM(2,2)),(N2Z,NORM(3,2))
      ICOL = 2
      IDEFPT (1) = 4
*    NORMAL TO RT. SHOULDER FLAP PLANE
      N1X = ZP(6) - ZP(4)
      N1Y = 0.
      N1Z = XP(4) - XP(6)
      IDEFPT(2) = 77
      N2X = 0.
      N2Y = 0.
      N2Z = -1.
      RETURN
      END


C    SUBROUTINE LSHFLP DEFINES SEGMENTING PLANES SEPARATING THE LEFT
C      SHOULDER FLAP FROM THE THORAX.
C
C
      SUBROUTINE LSHFLP
      IMPLICIT REAL (N)
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XP(78),YP(78),ZP(78)
      COMMON /PLACE/ ICOL
      EQUIVALENCE (NORM,N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z)
      EQUIVALENCE (N2X,NORM(1,2)),(N2Y,NORM(2,2)),(N2Z,NORM(3,2))
      ICOL = 2
      IDEFPT (1) = 3
*    NORMAL TO LT. SHOULDER FLAP PLANE
      N1X = ZP(3) - ZP(5)
      N1Y = 0.
      N1Z = XP(5) - XP(3)
      IDEFPT(2) = 78
      N2X = 0.
      N2Y = 0.
      N2Z = -1.
      RETURN
      END
```

```
*     SUBROUTINE RHFLP DEFINES SEGMENTING PLANES SEPARATING THE RIGHT HIP
C       FLAP FROM THE PELVIS.
C
C
      SUBROUTINE RHPFLP
      IMPLICIT REAL (N)
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XP(78),YP(78),ZP(78)
      COMMON /PLACE/ ICOL
      EQUIVALENCE (NORM,N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z)
      ICOL = 1
      IDEFPT(1) = 55
      N1X = ZP(55) - (ZP(54) + ZP(57))/2.
      N1Y = 0.
      N1Z = (XP(54) + XP(57))/2. - XP(55)
      RETURN
      END


C     SUBROUTINE LHFLP DEFINES SEGMENTING PLANES SEPARATING THE LEFT HIP
C       FLAP FROM THE PELVIS.
C
C
      SUBROUTINE LHPFLP
      IMPLICIT REAL (N)
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XP(78),YP(78),ZP(78)
      COMMON /PLACE/ ICOL
      EQUIVALENCE (NORM,N1X),(NORM(2,1),N1Y),(NORM(3,1),N1Z)
      EQUIVALENCE (N2X,NORM(1,2)),(N2Y,NORM(2,2)),(N2Z,NORM(3,2))
      ICOL = 2
      IDEFPT (1) = 55
      N1X = (ZP(53) + ZP(56))/2. - ZP(55)
      N1Y = 0.
      N1Z = XP(55) - (XP(53) +  XP(56))/2.
      IDEFPT (2) = 55
      N2X =  1.
      N2Y = 0.
      N2Z = 0.
      RETURN
      END
```

```
*    SUBROUTINE SORT2 CONTROLS PROCESSING OF CROSS SECTIONS WHICH ARE TO
C      HAVE DATA POINTS SEPARATED BETWEEN EITHER OF THE SHOULDER FLAPS
C      AND THE THORAX.  DATA POINTS BELONGING TO A SHOULDER FLAP ARE
C      STORED UNTIL THE LAST CROSS SECTION OF THE THORAX HAS BEEN PRO-
C      CESSED, AND ARE WRITTEN OUT AT THIS TIME.
C
C
      SUBROUTINE SORT2
      COMMON/POINTS/ X(99),Y(99),NPTS,Z
      COMMON /STORER/ DUM1(541),ISEGCT
      COMMON /PLACE/ DUM2(496),NPNLS(21),ISECT
      CALL LOOK (COLSG)
      IF (COLSG.EQ.0.) GOTO 200
      ISEGCT = ISEGCT +1
      WRITE (5,88) ISEGCT,NPTS,Z
      WRITE (5,99) (X(I),Y(I),I=1,NPTS)
      IF (ISEGCT.EQ.NPNLS(ISECT)) CALL UNSTOR
      RETURN
200   CALL SEP
      RETURN
88    FORMAT (1X,2I4,8X,F8.2)
99    FORMAT (1X,12F6.2)
      END



C    SUBROUTINE SORT CONTROLS THE PROCESSING OF CROSS SECTIONS WHICH ARE
C      TO HAVE DATA POINTS SEPARATED BETWEEN EITHER OF THE HIP FLAPS AND
C      THE PELVIS.  DATA POINTS BELONGING TO A HIP FLAP ARE STORED UNTIL
C      A CROSS SECTION WITH ALL DATA POINTS BELONGING TO THE HIP FLAP IS
C      ENCOUNTERED.  AT THIS POINT STORED HIP FLAP POINTS ARE WRITTEN OUT
C      OUT.
C
C
      SUBROUTINE SORT
      LOGICAL LSTSG
      COMMON /PLANE/ NORM(3,5),IDEFPT(5),XYZP(234),LSTSG
      COMMON /POINTS/ X(99),Y(99),NPTS,Z
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,250),ZSTOR(20),ISEGCT
     &,ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL,PDOT(99,5)

      CALL LOOK  (COLSG)
      IF  (COLSG) 300,200,100

300   IF (LSTSG) GOTO 100
      LSTSG = .TRUE.
      CALL UNSTOR

100   ISEGCT = ISEGCT +1
      WRITE (5,88) ISEGCT,NPTS,Z
      WRITE (5,99) (X(I),Y(I), I=1,NPTS)
      RETURN

200   CALL SEP
      RETURN

88    FORMAT (1X,2I4,8X,F8.2)
99    FORMAT (1X,12F6.2)
      END
```

```
*    SUBROUTINE LOOK EXAMINES THE COLUMN OF DOT PRODUCTS FOR A CROSS
C      SECTION. IF ALL DOT PRODUCTS ARE POSITIVE COLSG IS RETURNED WITH A
C      POSITIVE VALUE.  IF ALL ARE NEGATIVE COLSG IS RETURNED WITH A
C      NEGATIVE VALUE.  IF THE DOT PRODUCTS ARE OF MIXED SIGN COLSG IS
C      RETURNED AS 0. DOT PRODUCTS OF VALUE 0 ARE IGNORED IN THIS
C      EXAMINATION.
C
C
      SUBROUTINE LOOK  (COLSG)
      COMMON /POINTS/ DUM(198),NPTS
      COMMON /PLACE/ DUM2,PDOT(99)
      COLSG = PDOT(1)
      ISTRT = 2
10    IF (NPTS.LT.ISTRT) RETURN
      IF (COLSG.NE.0.) GOTO 50
      COLSG = PDOT(ISTRT)
      ISTRT = ISTRT +1
      GOTO 10
50    DO 100 I=ISTRT,NPTS
      IF (PDOT(I)*COLSG .GE. 0.) GOTO100
      COLSG = 0.
      RETURN
100   CONTINUE
      RETURN
      END
```

```
*    SUBROUTINE SEP IS CALLED FOR A CROSS SECTION WHICH HAS DOT PRODUCTS
C      OF MIXED SIGNS.  IT CONTROLS THE STORAGE OF DATA POINTS YIELDING
C      NEGATIVE DOT PRODUCTS, THE WRITING OF DATA POINTS WITH POSITIVE
C      DOT PRODUCTS, AND THE CREATION OF TWO NEW DATA POINTS.
C
C
       SUBROUTINE SEP
       REAL XYTEMP (2,99)
       LOGICAL SNGLPT
       COMMON /POINTS/ X(99),Y(99),NPTS,Z
       COMMON /PLACE/ ICOL,PDOT(99,5)
       COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR ( 500),ZSTOR(20),ISEGCT

       ITEMP = 0
       ISTRPL = ISTRPL +1
       IF (ISTRPL.GT.20) STOP "ISTOR AND ZSTOR UNDER DIMENSIONED IN FLAP"
       ZSTOR (ISTRPL) = Z
       ISTORE(ISTRPL) = 0
       SNGLPT = .FALSE.
       SIGN = PDOT (1)

       DO 100 I=1,NPTS
          IF (SIGN*PDOT(I).GT.0.) GOTO 50
          CALL ADDPT (I,ITEMP,XYTEMP)
          SIGN = PDOT(I)
          SNGLPT = .NOT.SNGLPT
50     IF (PDOT(I).LT.0.) GOTO 75
          CALL TEMPST (X(I), Y(I), ITEMP, XYTEMP)
          GOTO 100
75     CALL STORE (X(I),Y(I))
100    CONTINUE

       IF (SNGLPT) CALL ADDPT (1,ITEMP,XYTEMP)
       ISEGCT = ISEGCT +1
       WRITE (5,88) ISEGCT,ITEMP,Z
       WRITE (5,99) ((XYTEMP(I,J),I=1,2),J=1,ITEMP)

       RETURN
88     FORMAT (1X,2I4,8X,F8.2)
99     FORMAT (1X,12F6.2)
       END
```

```
*    SUBROUTINE ADDPT COMPUTES THE COORDINATES OF ONE OF THE PAIR OF
C      POINTS TO BE ADDED TO A CROSS SECTION WITH DOT PRODUCTS OF MIXED
C      SIGNS.
C
C
       SUBROUTINE ADDPT (I,ITEMP,XYTEMP)
       IMPLICIT REAL (N)
       REAL XYTEMP (198)
       INTEGER NPTS
       COMMON /POINTS/ X(99),Y(99),NPTS,Z
       COMMON /PLANE/ NORM(3,5),IDEFPT(5),XP(78),YP(78),ZP(78)
       ICOL = 1
       IF (Z.LT.ZP(55)) ICOL = 2
       C1 = X(I)
       C2 = Y(I)
       IF (I.EQ.1) GOTO 25
       B1 = X(I-1)
       B2 = Y(I-1)
       GOTO 50
25     B1 = X(NPTS)
       B2 = Y(NPTS)
50     N1 = NORM (1,ICOL)
       N2 = NORM (2,ICOL)
       N3 = NORM (3,ICOL)
       A1 = XP(IDEFPT(ICOL))
       A2 = YP(IDEFPT(ICOL))
       A3 = ZP(IDEFPT(ICOL))
       IF (B1.EQ.C1) GOTO 100
       SLOPE = (B2-C2)/(B1-C1)
       XADD = (N3*(A3 - Z) + N1*A1 + N2*(SLOPE*B1 + A2 - B2))
       XADD = XADD/(N1 + N2*SLOPE)
       YADD = SLOPE*(XADD - B1) + B2
       GOTO 150
100    XADD = B1
       YADD = (N1*(A1-B1) + N3*(A3-Z))/N2 + A2
150    CALL TEMPST (XADD,YADD,ITEMP,XYTEMP)
       CALL STORE (XADD,YADD)
       RETURN
       END
```

```
*    SUBROUTINE STORE STORES POINTS WITH NEGATIVE DOT PRODUCTS FROM A
C      CROSS SECTIONS HAVING DOT PRODUCTS OF BOTH SIGNS.
C
C
      SUBROUTINE STORE (X,Y)
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,250),DUM(21),ITOTST
      ITOTST = ITOTST +1
      IF (ITOTST.GT.250) STOP "XYSTOR UNDER DIMENSIONED IN FLAPS"
      XYSTOR (1,ITOTST) = X
      XYSTOR (2,ITOTST) = Y
      ISTORE(ISTRPL) = ISTORE(ISTRPL) +1
      RETURN
      END



C    SUBROUTINE TEMPST STORES DATA POINTS YIELDING POSITIVE DOT PRODUCTS
C      FROM A CROSS SECTION WITH DOT PRODUCTS OF MIXED SIGNS.  THESE
C      POINTS ARE STORED ONLY UNTIL THIS CROSS SECTION HAS BEEN COM-
C      PLETELY PROCESSED.
C
C
      SUBROUTINE TEMPST (X,Y,ITEMP,XYTEMP)
      REAL XYTEMP (2,99)
      ITEMP = ITEMP +1
      IF (ITEMP.GE.100) STOP"XYTEMP UNDER DIMENSIONED IN FLAPS"
      XYTEMP (1,ITEMP) = X
      XYTEMP (2,ITEMP) = Y
      RETURN
      END
```

```
*    SUBROUTINE UNSTOR IS CALLED WHEN A CROSS SECTION WITH ALL NEGATIVE
C      DOT PRODUCTS IS ENCOUNTERED.  IF DATA POINTS HAVE BEEN STORED
C      THEY ARE WRITTEN OUT BY UNSTOR.  ALSO VARIOUS COUNTERS ARE RESET.
C
C
      SUBROUTINE UNSTOR
      COMMON /STORER/ ISTRPL,ISTORE(20),XYSTOR(2,250),ZSTOR(20),ISEGCT,
     &ITOTST,NSEGCS(21),ISEG
      COMMON /PLACE/ ICOL

      ISEG = ISEG +1
      NSEGCS(ISEG) = ISEGCT
      ISEGCT = 0
      ISTRT = 1
      ISTP = 0

100   IF (ISEGCT.GE.ISTRPL) GOTO 200
      ISEGCT = ISEGCT +1
      ISTR = ISTORE (ISEGCT)
      WRITE (5,80) ISEGCT,ISTR,ZSTOR (ISEGCT)
      ISTP = ISTP +ISTR
      WRITE (5,99) ((XYSTOR(I,J),I=1,2),J=ISTRT,ISTP)
      ISTRT = ISTP +1
      GOTO 100

200   ISTRPL = ITOTST = 0
      ICOL = ICOL +1

      RETURN
80    FORMAT (1X,2I4,8X,F8.2)
99    FORMAT (1X,12F6.2)
      END



C    SUBROUTINE COMPRS IS USED TO COMBINE DOT PRODUCTS RESULTING FROM
C      MORE THAN ONE SEGMENTING PLANE. A 1 IS ASSIGNED IF THE POINT
C      BELONGS EITHER IN THE THORAX OR PELVIS, AND A -1 IS ASSIGNED IF
C      THE POINT BELONGS IN THE APPROPRIATE FLAP.
C
C
      SUBROUTINE COMPRS
      COMMON /PLACE/ ICOL,PDOT(99,5)
      COMMON /POINTS/ DUM1(198),NPTS
      DO 100 I=1,NPTS
      IF(PDOT(I,1).LT.0..AND.PDOT(I,2).LT.0.)  GOTO 75
      PDOT(I,1) = 1.
      GOTO 100
75    PDOT (I,1) = -1.
100   CONTINUE
      RETURN
      END
```

```
C     PROGRAM POLISH*******************************************************
C
C
C     PROGRAM POLISH IS THE THIRD IN A SERIES OF THREE SEGMENTATION
C     ROUTINES, USED TO REGROUP BODY SURFACE DESCRIPTION DATA POINTS INTO
C     DATA POINTS DESCRIBING THE SURFACE OF 19 DIFFERENT BODY SEGMENTS.
C     POLISH RECEIVES THE DATA OUTPUT BY THE SECOND RUN OF FLAPS, WHICH
C     HAS THE  DATA SEPARATED INTO TWENTY-ONE SEGMENTS.  POLISH PRODUCES A
C     HEADING FOR THIS DATA, COMBINES THE SHOULDER FLAPS WITH THE UPPER
C     ARM SEGMENTS, AND ADDS TWO CROSS SECTIONS BETWEEN THE THORAX AND
C     ABDOMEN AND TWO BETWEEN THE ABDOMEN AND PELVIS.
C
C     POLISH READS BODY SURFACE DESCRIPTION DATA POINTS FROM TAPE7.  IT
C     ALSO READS THE NUMBERS OF THE DATA SETS TO BE PROCESSED FROM TAPE3,
C     ALONG WITH THE NUMBER OF CROSS SECTION PER SEGMENT OF THE READ IN
C     DATA.  THE DATA POINTS RESULTING FROM THE PROCESSING OF POLISH ARE
C     WRITTEN TO TAPE5.


C     COMMON AREAS
C
C.../POINTS/--DATA PERTAINING TO THE CROSS SECTION PRESENTLY BEING PRO-
C        CESSED.
C     X--X COORDINATES FOR ALL POINTS IN THE CROSS SECTION.
C     Y--Y COORDINATES FOR ALL POINTS IN THE CROSS SECTION.
C     NPTS--NUMBER OF DATA POINTS IN THE CROSS SECTION.
C     Z--COMMON Z COORDINATE OF ALL POINTS IN THE CROSS SECTION.
C     JSTP--USED FOR COMMUNICATION BETWEEN ENTRY POINT COPY AND SUBROUTINE
C        ADDPT.
C     ZLEVEL--CONTAINS THE Z COORDINATES OF THE TWO CROSS SECTIONS TO BE
C        ADDED.
C
C.../PLACE/--DATA TO KEEP TRACK OF SEGMENT BEING PROCESSED.
C     NSEGCS--NUMBER OF CROSS SECTIONS PER SEGMENT OF DATA READ IN.
C     ISEG--NUMBER OF THE SEGMENT BEING PROCESSED.
C
C.../STORER/--DATA PERTAINING TO THE STORAGE OF DATA POINTS BELONGING TO
C        THE SHOULDER FLAPS.
C     XYSTOR--XY COORDINATES OF ALL STORED DATA POINTS.
C     ZSTOR--Z COORDINATES OF EACH CROSS SECTION WITH STORED DATA POINTS.
C     NPSTOR--CONTAINS THE NUMBER OF DATA POINTS IN EACH STORED CROSS SEC-
C        TION.
C     IISTRT--THE NEXT FREE ELEMENT IN XYSTOR.
C     IISTP--THE NUMBER OF CROSS SECTIONS STORED.
C
C.../FORM/--FORMATS USED BY SEVERAL ROUTINES.
C
C
C**********************************************************************
      PROGRAM POLISH (INPUT,OUTPUT,TAPE7,TAPE5,TAPE3)
      COMMON /POINTS/ X(99),Y(99),NPTS,Z,JSTP,ZLEVEL(2)
      COMMON /PLACE/ NSEGCS(21),ISEG
      COMMON /STORER/ XYSTOR(1200),ZSTOR(35),NPSTOR(35),IISTRT,IISTP
      COMMON /FORM/ NINE(2),EIGHT(2)
      DATA NINE /10H(1X,2I4,8X,6H,F8.2)/, EIGHT/10H(1X,12F6.2,1H)/

      READ (3,11) ISTRT,ISTP,INC
      DO 1000 ISUB=ISTRT,ISTP,INC
```

```
      ISEG = 0
      IISTRT = IISTP = 1
      WRITE (5,88) ISUB
      READ  (3,99) NSEGCS
      CALL LABEL
      CALL LMARK
      CALL SKIP (3)
      CALL STORE (2)
      CALL ADDPL
      CALL STORE (2)
      IISTRT = IISTP = 1
      CALL COMB (4)
      CALL SKIP (2)
      CALL COMB (5)
      CALL SKIP (2)
      CALL COMB (8)
      CALL SKIP (3)
      CALL COMB (9)
      CALL SKIP (3)
      ENDFILE 5
1000  CONTINUE
      STOP "FROM POLISH"
11    FORMAT (3I5)
88    FORMAT (*1*,31X,*SUBJECT NUMBER*,I3)
99    FORMAT (4X,21I3)
      END
```

```
*    SUBROUTINE LMARK READS IN THE LANDMARK COORDINATES, AND WRITES THEM
C      BACK OUT WITH NAMES.  ADDITIONALLY IT STORES THE Z COORDINATES OF
C      LANDMARKS 7 AND 52, WHICH DEFINE THE SEPARATION BETWEEN THE THORAX
C      AND ABDOMEN, AND ABDOMEN AND PELVIS RESPECTIVELY.
C
C
      SUBROUTINE LMARK
      COMMON /POINTS/ DUM(201),ZLEVEL(2)
      DIMENSION IMARK(2),CARD(4),LMKNM(2,77)
      DATA IMARK/7,52/
      DATA((LMKNM(I,J),I=1,2),J=1,26) /
     &          10HNUCHALE   ,10H          ,10HCERVICALE ,10H          ,
     &          10HLEFT ACROM,10HIALE      ,10HRIGHT ACRO,10HMIALE     ,
     &          10HLEFT POS S,10HCYE       ,10HRIGHT POS ,10HSCYE      ,
     &          10H10TH RIBMI,10HDSPINE    ,10HPOS SUP IL,10HIAC MS    ,
     &          10HL MED HUM ,10HEPICON    ,10HR MED HUM ,10HEPICON    ,
     &          10HL LAT HUM ,10HEPICON    ,10HR LAT HUM ,10HEPICON    ,
     &          10HLEFT OLECR,10HANON      ,10HRIGHT OLEC,10HRANON     ,
     &          10HLEFT RADIA,10HLE        ,10HRIGHT RADI,10HALE       ,
     &          10HL GLUTEAL ,10HFOLD      ,10HR GLUTEAL ,10HFOLD      ,
     &          10HL ULNAR ST,10HYLOID     ,10HR ULNAR ST,10HYLOID     ,
     &          10HL RADIAL S,10HTYLOID    ,10HR RADIAL S,10HTYLOID    ,
     &          10HL METACARP,10HALE II    ,10HR METACARP,10HALE II    ,
     &          10HL METACARP,10HALEIII    ,10HR METACARP,10HALEIII    /
      DATA((LMKNM(I,J),I=1,2),J=27,52) /
     &          10HL METACARP,10HALE V     ,10HR METACARP,10HALE V     ,
     &          10HLEFT DACTY,10HLION      ,10HRIGHT DACT,10HYLION     ,
     &          10HL POS CALC,10HANEUS     ,10HR POS CALC,10HANEUS     ,
     &          10HHEAD CIRC ,10H          ,10HSELLION   ,10H          ,
     &          10HL INFRAORB,10HITALE     ,10HR INFRAORB,10HITALE     ,
     &          10HLEFT TRAGI,10HON        ,10HRIGHT TRAG,10HION       ,
     &          10HLEFT GONIO,10HN         ,10HRIGHT GONI,10HON        ,
     &          10HMID THYROI,10HD CART    ,10HLEFT CLAVI,10HCALE      ,
     &          10HRIGHT CLAV,10HICALE     ,10HSUPRASTERN,10HALE       ,
     &          10HLEFT ANT S,10HCYE       ,10HRIGHT ANT ,10HSCYE      ,
     &          10HLEFT BUSTP,10HOINT      ,10HRIGHT BUST,10HPOINT     ,
     &          10HLEFT 10TH ,10HRIB       ,10HRIGHT 10TH,10H RIB      ,
     &          10HL ILIOCRIS,10HTALE      ,10HR ILIOCRIS,10HTALE      /
      DATA((LMKNM(I,J),I=1,2),J=53,77) /
     &          10HLEFT ASIS ,10H          ,10HRIGHT ASIS,10H          ,
     &          10HSYMPHYSION,10H          ,10HL TROCHANT,10HERION     ,
     &          10HR TROCHANT,10HERION     ,10HL LAT FEM ,10HCONDYL    ,
     &          10HR LAT FEM ,10HCONDYL    ,10HL MED FEM ,10HCONDYL    ,
     &          10HR MED FEM ,10HCONDYL    ,10HLEFT TIBIA,10HLE        ,
     &          10HRIGHT TIBI,10HALE       ,10HLEFT FIBUL,10HARE       ,
     &          10HRIGHT FIBU,10HLARE      ,10HL LAT MALL,10HEOLUS     ,
     &          10HR LAT MALL,10HEOLUS     ,10HLEFT SPHYR,10HION       ,
     &          10HRIGHT SPHY,10HRION      ,10HL METATARS,10HAL I      ,
     &          10HR METATARS,10HAL I      ,10HL METATARS,10HAL V      ,
     &          10HR METATARS,10HAL V      ,10HLEFT TOE I,10HI         ,
     &          10HRIGHT TOE ,10HII        ,10HCROTCH SEN,10HSOR       ,
     &          10H(42 + 43)/,10H2
      ICNT = 1
      DO 100 I=1,76
      IF (I.EQ.IMARK(ICNT)) GOTO 75
      READ (7,99) CARD
      WRITE (5,66) CARD(1),(LMKNM(J,I),J=1,2),(CARD(J),J=2,4)
      GOTO 100
75    READ (7,88) II,X,Y,ZLEVEL(ICNT)
      WRITE (5,77) II,(LMKNM(J,I),J=1,2),X,Y,ZLEVEL(ICNT)
      ICNT = ICNT +1
100   CONTINUE
```

```
      READ (7,77)
      READ (7,77)
      RETURN
66    FORMAT (A5,5X,5A10)
77    FORMAT (I5,5X,2A10,3F10.2)
88    FORMAT    (I5,3F10.2)
99    FORMAT (A5,3A10)
      END


C   SUBROUTINE SKIP IS USED TO SKIP OVER NSEG SEGMENTS WHICH REQUIRE
C     NO PROCESSING.
C
C
      SUBROUTINE SKIP (NSEG)
      COMMON /POINTS/ X(99),Y(99),NPTS,Z,JSTP
      COMMON /PLACE/ NSEGCS(21),ISEG
      COMMON /FORM / NINE(2),EIGHT(2)
      JSTRT = 1
      GOTO 10
      ENTRY COPY
      JSTRT = NSEG +1
      NSEG =1
10    DO 100 I=1,NSEG
      ISEG = ISEG +1
      JSTP = JSTRT + NSEGCS(ISEG) -1
50    DO 100 J = JSTRT,JSTP
      READ (7,NINE) IPLANE,NPTS,Z
      WRITE (5,NINE) J,NPTS,Z
      READ (7,EIGHT) (X(II),Y(II),II=1,NPTS)
      WRITE (5,EIGHT) (X(II),Y(II),II=1,NPTS)
100   CONTINUE
      RETURN
      END
```

AD-A114 916 DAYTON UNIV OH RESEARCH INST F/G 6/2
SEGMENTATION AND ANALYSIS OF STEREOPHOTOMETRIC BODY SURFACE DAT--ETC(U)
APR 82 L D BAUGHMAN F33615-78-C-0504
UNCLASSIFIED UDR-TR-81-51 AFAMRL-TR-81-96 NL

2 OF 3
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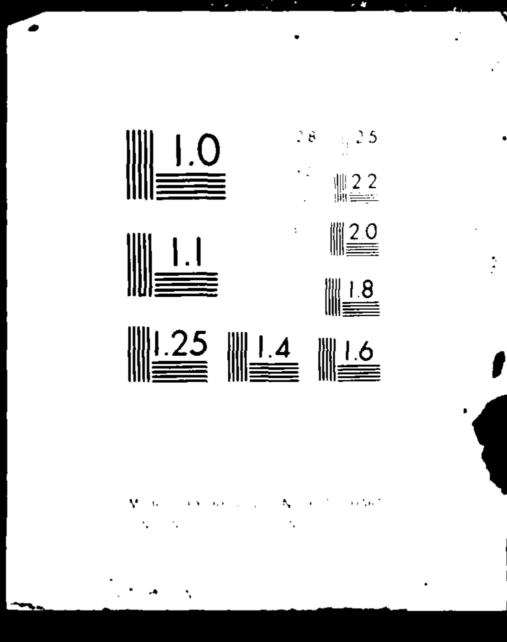

```
*    SUBROUTINE LABEL WRITES OUT SEGMENT NAMES AND THE NUMBER OF CROSS
C      SECTIONS PER SEGMENT AFTER PROCESSING BY POLISH.
C
C
      SUBROUTINE LABEL
      COMMON /PLACE/ NSEGCS(21)
      DIMENSION SEGNM(19)
      DATA SEGNM /4HHEAD,4HNECK,6HTHORAX,7HABDOMEN,6HPELVIS,6HR FLAP,6HL
     & FLAP,6HRU ARM,6HRF ARM,6HR HAND,6HLU ARM,6HLF ARM,6HL HAND,
     &7HR THI-F,6HR CALF,6HR FOOT,7HL THI-F,6HL CALF,6HL FOOT /
      CALL WRTR ( 1, 2,0,SEGNM)
      WRITE (5,99) SEGNM(3),NSEGCS(3 ) +1
      WRITE (5,99) SEGNM(4),NSEGCS(6 ) +2
      WRITE (5,99) SEGNM(5),NSEGCS(7 ) +1
      WRITE (5,99) SEGNM(8),NSEGCS(10) + NSEGCS(4)
      CALL WRTR ( 9,10,2,SEGNM)
      WRITE (5,99) SEGNM(11),NSEGCS(13) + NSEGCS(5)
      CALL WRTR (12,13,2,SEGNM)
      WRITE (5,99) SEGNM(6),NSEGCS(8 )
      CALL WRTR (14,16,2,SEGNM)
      WRITE (5,99) SEGNM(7),NSEGCS(9 )
      CALL WRTR (17,19,2,SEGNM)
      RETURN
99    FORMAT (A15,I15)
      END


C    SUBROUTINE WRTR IS CALLED BY LABEL TO WRITE OUT THE NAME OF AND NUM-
C      BER OF CROSS SECTIONS PER SEGMENT FOR SEGMENTS ISTRT THROUGH ISTP.
C
C
      SUBROUTINE WRTR (ISTRT,ISTP,IOFF,SEGNM)
      COMMON /PLACE/ NSEGCS(21)
      DIMENSION SEGNM (19)
      DO 100 I = ISTRT,ISTP
100   WRITE (5,99) SEGNM(I),NSEGCS(I + IOFF)
      RETURN
99    FORMAT (A15,I15)
      END
```

```
*     SUBROUTINE STORE IS CALLED TO STORE DATA POINTS BELONGING TO THE
C       SHOULDER FLAPS.
C
C
      SUBROUTINE STORE (NSEG)
      COMMON /STORER/ XYSTOR(1200),ZSTOR(35),NPSTOR(35),IISTRT,IPLSTR
      COMMON /PLACE/ NSEGCS(21),ISEG
      COMMON /FORM/ NINE(2),EIGHT(2)
      NPL = IPLSTR -1
      DO 100 I = 1,NSEG
      ISEG = ISEG +1
100   NPL = NPL + NSEGCS(ISEG)
      IF (NPL.GT.35) STOP "ZSTOR AND NPSTOR UNDER DIMENSIONED IN POLISH"
      DO 200 I = IPLSTR,NPL
      READ (7,NINE) IPL,NPSTOR(I),ZSTOR(I)
      IISTP = IISTRT + 2*NPSTOR(I) -1
      IF (IISTP.GT.1200) STOP "XYSTOR UNDER DIMENSIONED IN POLISH"
      READ (7,EIGHT) (XYSTOR(II),II = IISTRT,IISTP)
200   IISTRT = IISTP +1
      IPLSTR = NPL +1
      RETURN
      END


C     SUBROUTINE COMB COMBINES THE CROSS SECTIONS OF A SHOULDER FLAP WITH
C       THE APPROPRIATE UPPER ARM SEGMENT.
C
C
      SUBROUTINE COMB (ISEG)
      COMMON /PLACE/ NSEGCS(21)
      COMMON /STORER/ XYSTOR(1200),ZSTOR(35),NPSTOR(35),IPLSTR,IPTSTR
      COMMON /FORM/ NINE(2),EIGHT(2)
      NPL = NSEGCS(ISEG)
      DO 100 I = 1,NPL
      NPTS = NPSTOR(IPLSTR)
      WRITE (5,NINE) I,NPTS,ZSTOR(IPLSTR)
      IPTSTP = IPTSTR + 2*NPTS -1
      WRITE (5,EIGHT) (XYSTOR(II),II=IPTSTR,IPTSTP)
      IPLSTR = IPLSTR +1
100   IPTSTR = IPTSTP +1
      IF (ISEG.LT.6)  CALL COPY (NPL)
      RETURN
      END
```

```
*     SUBROUINE ADDPL CONTROLS THE CREATION OF 2 NEW CROSS SECTIONS AND
C       THEIR WRITING OUT.
C
C
        SUBROUTINE ADDPL
        COMMON /POINTS/ X(99),Y(99),NPTS,Z,IPNL,ZLEVEL(2)
        COMMON /FORM/ NINE(2),EIGHT(2)
        DIMENSION X2(75),Y2(75),A(75),B(75)
        DO 100 I = 1,2
        READ (7,NINE) IPL,NP2,Z2
        READ (7,EIGHT) (X2(II),Y2(II),II=1,NP2)
        JSTP =  NP2/6
        IF ( 6*JSTP.LT.NP2)  JSTP = JSTP +1
        JSTP = JSTP +1
        DO 90 J=1,JSTP
        BACKSPACE 7
90      CONTINUE
        CALL INTPNL (X,Y,Z,NPTS,X2,Y2,Z2,NP2,A,B,ZLEVEL(I),NPAB)
        WRITE (5,NINE) IPNL +1,NPAB,ZLEVEL(I)
        WRITE (5,EIGHT) (A(II),B(II),II=1,NPAB)
        WRITE (5,NINE )     IPL,NPAB,ZLEVEL(I)
        WRITE (5,EIGHT) (A(II),B(II),II=1,NPAB)
        CALL COPY (IPL)
100     CONTINUE
        RETURN
        END



C     SUBROUTINE INTPNL CONTROLS THE CREATION OF A CROSS SECTION.  THE
C       CROSS SECTION IMMEDIATELY ABOVE THE ONE BEING CREATED IS DESCRIBED
C       BY THE FIRST FOUR PARAMETERS, THE ONE IMMEDIATELY BELOW IS
C       DESCRIBED BY THE NEXT FOUR PARAMETERS.
C
C
        SUBROUTINE INTPNL (X1,Y1,Z1,NP1,X2,Y2,Z2,NP2,A1,B1,ZAB,NPAB)
        DIMENSION X1(NP1),Y1(NP1),X2(NP2),Y2(NP2),A1(99),B1(99),
       &B2(99),ANG1(198),RAD1(198),ANG2(198),RAD2(198),THTA(99)
        DATA TWOPI/6.283185300/
        CALL WEIGHT (Z1,Z2,ZAB,WT1,WT2)
        X0 = Y0 = 0.
        CALL SUMXY (X1,Y1,NP1,X0,Y0,WT1/FLOAT(NP1))
        CALL SUMXY(X2,Y2,NP2,X0,Y0,WT2/FLOAT(NP2))
        NPAB = IFIX(WT1*FLOAT(NP1) + WT2*FLOAT(NP2) + .5)
        CALL POLAR (X1,Y1,X0,Y0,NP1,ANG1(50),RAD1(50))
        CALL POLAR (X2,Y2,X0,Y0,NP2,ANG2(50),RAD2(50))
        THTA (1) = WT1*ANG1(50) + WT2*ANG2(50)
        RINC = TWOPI/FLOAT(NPAB)
        DO 10 I = 2,NPAB
10      THTA(I) = THTA(I-1) + RINC
        CALL INTER (ANG1,RAD1,NP1,THTA,B1,NPAB)
        CALL INTER (ANG2,RAD2,NP2,THTA,B2,NPAB)
        DO  100 I=1,NPAB
100     B1(I) = WT1*B1(I) + WT2*B2(I)
        CALL RECT (THTA,B1,A1,NPAB,X0,Y0)
        RETURN
        END
```

```
*    SUBROUTINE WEIGHT COMPUTES WEIGHT FACTORS TO BE USED IN WEIGHTED
C      AVERAGES FOR CROSS SECTION CREATION.
C
C
       SUBROUTINE WEIGHT (Z1,Z2,ZAB,WT1,WT2)
       WT1 = Z1 - Z2
       WT2 = (Z1 - ZAB)/WT1
       WT1 = (ZAB - Z2)/WT1
       RETURN
       END



C    SUBROUTINE SUMXY ADDS X AND Y TO X0 AND Y0, RESPECTIVELY WITH A
C      WEIGHT FACTOR.
C
C
       SUBROUTINE SUMXY (X,Y,N,X0,Y0,WT)
       DIMENSION X(N),Y(N)
       DO 100 I = 1,N
       X0 = X0 + WT*X(I)
100    Y0 = Y0 + WT*Y(I)
       RETURN
       END
```

```
*    SUBROUTINE POLAR COMPUTES THE POLAR COORDINATES OF EACH X,Y PAIR IN
C      PARAMETERS X AND Y, RELATIVE TO THE PARAMETERS X0,Y0.  IT ALSO
C      ORDERS THE RESULTING POLAR COORDINATES BY ASCENDING ANGLE, AND
C      REMOVES ANY POINT THAT IS A DUPLICATE.
C
C
      SUBROUTINE POLAR (X,Y,X0,Y0,N,ANG,RAD)
      DIMENSION X(N),Y(N),ANG(99),RAD(99),IR(99)
      DATA TWOPI/6.283185308/
      DO 10  I=1,N
      XP = X(I) - X0
      YP = Y(I) - Y0
      RAD(I) = SQRT(XP**2 + YP**2)
      IF (RAD(I) .EQ.0.) STOP "RADIUS OF LENGTH 0. IN POLAR"
      ANG(I) = ATAN2(YP,XP)
10    IR(I) = I
C
C    SUBROUTINES VSRTR AND VSTRU ARE FORM THE IMSL LIBRARY, AND USED TO
C      ORDER THE RESULTING POLAR COORDINATES.
      CALL VSRTR (ANG,N,IR)
      CALL VSRTU (RAD,1,1,N,0,IR,WK)
      ISTRT = 1
      ANGLST = ANG(N) - TWOPI
50    DO 100 I=ISTRT,N
      IF (ANG(I).EQ.ANGLST) GOTO 200
100   ANGLST = ANG(I)
      RETURN
200   ISTRT = I
      N = N -1
      IF (ISTRT.GT.N) RETURN
      DO 300 I=ISTRT,N
      ANG(I) = ANG(I+1)
300   RAD(I) = RAD(I+1)
      GOTO 50
      END
```

```
*   SUBROUTINE INTER EXTENDS THE POLAR DATA POINTS 1/2 PERIOD TO THE
C     LEFT AND RIGHT.  IT THEN FITS A SPLINE TO THESE DATA POINTS, AND
C     EVALUATES IT AT THE ANGLES SPECIFIED IN PARAMETER THTA.  THE RE-
C     SULTS ARE CONVERTED TO RECTILINEAR COORDINATES AND RETURNED IN
C     PARAMETERS A AND B.
C
C
      SUBROUTINE INTER (ANG,RAD,NP,THTA,B,NPAB)
      DIMENSION ANG(198),RAD(198),THTA(NPAB),B(NPAB),C(197,3),BPAR(4)
      DATA TWOPI/6.283185308/,IC/197/
      ISTRT = 50 + NP
      ISTP = ISTRT + NP/2
      DO 100 I = ISTRT,ISTP
      ANG(I) = ANG(I-NP) + TWOPI
100   RAD(I) = RAD(I-NP)
      ISTRT = 50 -  NP + ISTP - ISTRT + 1
      DO 110 I=ISTRT,49
      ANG(I) = ANG(I+NP) - TWOPI
110   RAD(I) = RAD(I+NP)
      ISTP = ISTRT + 2*NP -1
      CALL DERIV (ANG(ISTRT),RAD(ISTRT),2*NP,FPX1,FPXN)
      BPAR(1) = BPAR(3) = 1.
      BPAR(2) = 6.*(RAD(ISTRT+1) - RAD(ISTRT))/
     &              (ANG(ISTRT+1) - ANG(ISTRT))**2 - FPX1
      BPAR(4) = (6.*FPXN - RAD(ISTP) + RAD(ISTP -1))/
     &            (ANG(ISTP) - ANG(ISTP -1))
C
C   SUBROUTINES ICSICU AND ICSEVU ARE FROM THE IMSL LIBRARY, AND ARE
C     USED TO FIT AND EVALUATE THE SPLINE.
      CALL ICSICU (ANG(ISTRT),RAD(ISTRT),NP*2,BPAR,C,IC,IER)
      CALL ICSEVU (ANG(ISTRT),RAD(ISTRT),NP*2,C,IC,THTA,B,NPAB)
      RETURN
      END



C   SUBROUTINE RECT CONVERTS THE POLAR COORDINATE PAIRS (THTA,B) TO
C     RECTILINEAR COORDINATE PAIRS (A,B) RELATIVE TO (X0,Y0).
C
C
      SUBROUTINE RECT (THTA,B,A,NPAB,X0,Y0)
      DIMENSION THTA(NPAB),B(NPAB),A(NPAB)
      DO 100 I=1,NPAB
      A(I) = B(I)*COS(THTA(I)) + X0
100   B(I) = B(I)*SIN(THTA(I)) + Y0
      RETURN
      END
```

```
*    SUBROUTINE DERIV IS CALLED BY INTER TO SUPPLY VALUES FOR THE DERIV-
C      ATIVE OF THE SPLINE AT ITS END POINTS.
C
C
       SUBROUTINE DERIV (X,Y,NP,FPX1,FPXN)
       DIMENSION X(NP),Y(NP)
       DATA TWOPI/6.283185308/
       X0 = X(NP/2) - TWOPI
       Y0 = Y(NP/2)
       CALL FP (X0,Y0,X(1),Y(1),X(2),Y(2),FPX1)
       X0 = X(NP/2 + 1) + TWOPI
       Y0 = Y(NP/2 + 1)
       CALL FP (X(NP-1),Y(NP-1),X(NP),Y(NP),X0,Y0,FPXN)
       RETURN
       END



C    SUBROUTINE FP IS USED TO CALCULATE THE DERIVATIVE OF THE PARABOLA
C      PASSING THROUGH (X1,Y1), (X2,Y2), AND (X3,Y3), EVALUATED AT
C      (X2,Y2).
C
C
       SUBROUTINE FP (X1,Y1,X2,Y2,X3,Y3,FPX2)
       DEN1 = (X1-X2) * (X1-X3)
       DEN2 = (X2-X1) * (X2-X3)
       DEN3 = (X3-X1) * (X3-X2)
       FPX2 = 2*X2 * (Y1/DEN1 + Y2/DEN2 + Y3/DEN3)
       FPX2 = FPX2 - (X2 + X3)*Y1/DEN1 - (X1 + X3)*Y2/DEN2
      &           - (X1 + X2)*Y3/DEN3
       RETURN
       END
```

APPENDIX G

SAMPLE OF DATA PRODUCED BY SEGMENTATION ROUTINES

This appendix lists the final output of the segmentation routines (i.e., the output of program POLISH) for the eleventh data set. This illustrates the header produced by program POLISH, as well as the cross section format used for the stereophotometric data.

The first line of each of these data sets gives the number associated with the subject for which the data was prepared. The next 19 lines give the number of cross sections each segment contains. These 19 lines also reflect the order in which cross section data are arranged (i.e., cross sections with data points belonging to the head first, followed by cross sections associated with the neck, etc.). The 76 lines following list the landmark points and their locations. These locations are relative to the axis system used by TIRR (Z upward, X and Y approximately to the subject's right and front, respectively, and coordinates measured in centimeters).

The lines mentioned above form the header produced by program POLISH. Following these lines is the body of the data consisting of the body surface data points, listed by cross section. The format used for this portion of the data set is consistent between the TIRR data, and the data output at each stage of segmentation. As mentioned, the body surface data points are grouped by horizontal cross section. The first line for each set of data describing a cross section gives the cross section number, number of data points in the cross section, and common Z coordinate of all data points in the cross section (in that order). After this line follows the X, Y coordinates of all data points in the cross section, with up to six X, Y pairs per line. As with the landmarks the coordinates of the data points are relative to the axis system used by TIRR.

SUBJECT NUMBER 11

HEAD	12
NECK	7
THORAX	20
ABDOMEN	3
PELVIS	11
RU ARM	16
RF ARM	11
R HAND	10
LU ARM	16
LF ARM	12
L HAND	10
R FLAP	8
R THI-F	15
R CALF	21
R FOOT	4
L FLAP	7
L THI-F	15
L CALF	21
L FOOT	4

1	NUCHALE	46.92	-9.20	156.65
2	CERVICALE	46.93	-7.62	147.42
3	LEFT ACROMIALE	28.42	-6.25	139.72
4	RIGHT ACROMIALE	65.70	-5.87	139.49
5	LEFT POS SCYE	31.76	-11.20	128.63
6	RIGHT POS SCYE	62.67	-10.71	128.41
7	10TH RIBMIDSPINE	46.70	-8.99	108.13
8	POS SUP ILIAC MS	47.07	-10.79	101.02
9	L MED HUM EPICON	28.21	-.10	108.05
10	R MED HUM EPICON	66.09	.49	106.82
11	L LAT HUM EPICON	23.41	-5.94	109.89
12	R LAT HUM EPICON	70.94	-5.62	109.16
13	LEFT OLECRANON	27.61	-4.70	108.79
14	RIGHT OLECRANON	66.18	-4.55	107.97
15	LEFT RADIALE	23.44	-5.33	108.06
16	RIGHT RADIALE	70.97	-5.34	107.17
17	L GLUTEAL FOLD	39.45	-11.93	77.01
18	R GLUTEAL FOLD	55.89	-12.70	77.71
19	L ULNAR STYLOID	15.99	-2.60	85.27
20	R ULNAR STYLOID	79.27	-2.39	84.37
21	L RADIAL STYLOID	10.32	-2.72	86.53
22	R RADIAL STYLOID	84.01	-2.43	86.14
23	L METACARPALE II	6.21	-1.94	79.12
24	R METACARPALE II	88.48	-1.41	79.19
25	L METACARPALEIII	9.33	-3.04	77.35
26	R METACARPALEIII	85.68	-1.69	77.06
27	L METACARPALE V	14.10	-.45	77.97
28	R METACARPALE V	80.92	.61	77.21
29	LEFT DACTYLION	6.01	-1.23	67.99
30	RIGHT DACTYLION	88.97	.60	67.85
31	L POS CALCANEUS	34.38	-12.77	1.22
32	R POS CALCANEUS	59.56	-13.62	1.21
33	HEAD CIRC	47.10	8.01	165.60
34	SELLION	47.02	8.57	161.99
35	L INFRAORBITALE	42.93	7.04	160.31
36	R INFRAORBITALE	47.56	6.94	160.12
37	LEFT TRAGION	39.89	-.29	158.84
38	RIGHT TRAGION	54.22	-.45	158.80
39	LEFT GONION	41.50	.76	153.10
40	RIGHT GONION	52.69	.55	153.16
41	MID THYROID CART	46.97	3.08	146.85
42	LEFT CLAVICALE	44.23	2.61	142.83
43	RIGHT CLAVICALE	49.71	2.60	142.76
44	SUPRASTERNALE	46.94	3.47	141.59
45	LEFT ANT SCYE	31.36	.75	128.26
46	RIGHT ANT SCYE	62.65	1.11	128.42
47	LEFT BUSTPOINT	37.40	13.57	125.04
48	RIGHT BUSTPOINT	56.50	13.89	124.75
49	LEFT 10TH RIB	34.33	-1.82	109.11
50	RIGHT 10TH RIB	60.13	-1.95	108.90
51	L ILIOCRISTALE	32.13	-.70	104.91
52	R ILIOCRISTALE	61.69	-1.61	106.39
53	LEFT ASIS	35.09	8.03	94.72
54	RIGHT ASIS	60.42	7.10	95.27
55	SYMPHYSION	47.45	9.30	86.95
56	L TROCHANTERION	29.62	.09	88.81
57	R TROCHANTERION	65.79	-2.26	89.07
58	L LAT FEM CONDYL	32.75	-5.69	48.81
59	R LAT FEM CONDYL	62.63	-4.97	48.67
60	L MED FEM CONDYL	44.00	-6.70	47.30
61	R MED FEM CONDYL	51.27	-4.75	47.29
62	LEFT TIBIALE	42.11	-5.47	44.33

```
 63     RIGHT TIBIALE                 52.90      -4.19      44.20
 64     LEFT FIBULARE                 32.03      -0.00      44.31
 65     RIGHT FIBULARE                62.95      -6.09      44.53
 66     L LAT MALLEOLUS               31.45      -0.01       7.24
 67     R LAT MALLEOLUS               62.41      -9.72       7.00
 68     LEFT SPHYRION                 37.29      -4.76       6.71
 69     RIGHT SPHYRION                56.34      -5.99       6.31
 70     L METATARSAL I                30.23       5.57       2.33
 71     R METATARSAL I                56.79       5.31       2.27
 72     L METATARSAL V                29.02       3.36        .90
 73     R METATARSAL V                65.63       2.22        .60
 74     LEFT TOE II                   34.20      11.70        .12
 75     RIGHT TOE II                  61.81      11.09        .40
 76     CROTCH SENSOR                 47.49       2.24      79.20
  1   1             173.07
47.50  1.31
  2  15             171.93
43.03 -6.09 45.07 -7.22 46.39 -7.72 47.00 -7.84 48.87 -7.91 49.65 -7.30
50.39 -6.47 50.87 -5.92 50.87  1.03 49.62  2.06 48.34  3.10 46.70  3.29
44.96  2.51 44.01  1.51 43.47   .75
  3  20             169.90
41.49 -5.40 42.45 -6.70 44.00 -8.20 45.93 -9.40 48.20 -9.59 50.00 -9.19
51.82 -8.06 52.74 -6.83 53.33 -5.73 53.46 -5.33 53.45  -.04 52.87  1.42
52.07  2.64 50.67  4.21 48.59  5.55 46.46  5.61 44.16  4.83 42.57  3.25
41.70  1.76 41.30  1.04
  4  22             167.90
40.12 -4.99 40.70 -6.32 41.80 -7.96 43.63 -9.79 45.56-10.44 47.72-10.70
50.64 -9.99 52.60 -8.76 53.70 -7.50 54.49 -6.15 54.76 -4.82 54.56  -.24
53.67  1.73 52.51  4.07 50.44  6.06 48.37  7.21 45.72  7.07 43.16  5.96
41.53  3.05 40.54  1.09 39.89  -.22 39.70  -.79
  5  20             165.90
39.55 -4.92 40.03 -6.33 40.07 -7.79 42.10 -9.25 43.76-10.43 45.47-11.17
47.52-11.29 50.40-10.97 52.31 -9.60 53.72 -8.49 54.86 -6.90 55.30 -5.17
55.60 -4.14 55.46  -.55 55.02  1.29 54.07  3.37 52.97  5.21 51.30  6.69
49.65  7.50 47.92  8.01 46.17  8.01 44.77  7.63 43.29  6.87 42.00  5.81
40.71  4.05 39.73  1.91 39.29  -.17 39.00  -.91
  6  20             163.93
39.59 -6.02 40.41 -7.73 41.73 -9.05 44.05-11.06 46.27-11.50 48.61-11.54
51.15-10.99 53.39 -9.40 54.20 -8.11 54.94 -6.33 55.57 -4.66 55.05 -3.51
55.89 -3.14 55.60  -.76 55.10  1.29 54.42  3.22 52.96  5.81 51.52  7.31
49.32  8.01 46.95  8.33 44.93  8.10 43.63  7.73 42.25  6.05 41.33  5.79
40.44  4.00 39.73  2.30 39.13   .44 38.07  -.40
  7  31             161.91
38.96 -3.16 39.32 -4.63 40.09 -6.95 41.45 -8.70 43.43-10.81 46.10-11.94
40.02-11.66 51.09-10.81 52.73 -9.00 53.06 -8.53 54.07 -6.07 55.40 -4.77
55.50 -3.73 55.67 -2.95 55.32  -.87 55.00  1.44 54.33  3.47 53.25  5.43
51.76  6.60 49.99  7.26 48.07  7.14 47.89  8.36 46.96  8.63 45.96  7.90
44.93  7.02 43.84  7.12 42.22  6.44 40.60  4.92 39.00  3.00 39.34  1.39
39.07  -.56
  8  36             159.92
38.34 -2.98 38.77 -3.22 39.21 -3.05 39.36 -3.73 39.86 -5.55 40.72 -7.39
43.11 -9.82 45.90-11.33 48.08-11.32 50.12-10.84 52.21-10.02 53.55 -8.45
54.55 -5.69 55.04 -3.60 55.49 -3.55 55.95 -3.32 56.10 -2.26 55.44  -.03
55.03  1.10 54.20  3.94 53.19  5.61 51.40  7.10 49.90  7.40 48.65  8.12
47.00  9.07 46.90  9.96 46.05  9.73 45.37  8.71 44.25  7.61 42.40  7.00
41.07  5.00 39.84  3.09 39.40  1.67 38.99  -.22 38.60 -1.91 38.20 -2.52
  9  30             157.94
38.71 -3.34 39.36 -3.41 39.83 -3.26 40.35 -4.44 40.99 -6.55 42.10 -8.29
43.99 -9.62 45.64-10.11 47.47-10.44 49.03-10.36 50.89 -9.79 52.44 -8.45
53.38 -6.60 54.29 -4.87 54.63 -3.40 55.07 -3.63 55.47 -3.45 55.23 -2.32
54.43 -1.33 54.43  2.27 53.66  4.97 52.26  6.89 50.67  8.00 49.15  8.21
48.50  9.19 47.90  9.49 47.19 10.36 46.49 10.00 46.06  9.01 45.43  9.07
44.42  8.11 43.29  7.96 41.70  6.03 40.70  5.42 39.95  3.42 39.60  -.14
39.20 -1.47 38.77 -2.47
 10  30             155.96
39.20 -1.00 39.71 -1.09 40.35 -1.53 40.94 -1.67 41.00 -3.00 41.71 -5.00
43.14 -6.47 43.06 -7.25 50.70 -7.20 51.12 -7.05 52.40 -5.67 53.23 -4.05
53.53 -2.15 53.00 -2.14 54.39 -2.40 54.05 -2.55 54.05 -2.55 54.72  -.65
53.97   .25 53.90  2.57 52.59  5.50 50.07  8.02 47.57  9.40 45.90  9.30
43.75  8.20 41.65  7.01 40.62  5.03 40.14  2.00 39.70   .21 39.40  -.39
 11  16             153.95
41.06 -1.59 41.06 -1.61 53.31 -1.67 53.61  1.61 53.30  3.30 52.16  5.09
50.57  7.29 48.70  8.45 47.16  9.22 45.21  8.96 43.42  7.74 42.23  6.69
41.12  5.31 40.60  3.29 40.63  1.63 40.63  1.63
 12   8             151.90
51.77  4.00 51.44  5.47 50.11  7.32 48.22  8.62 45.70  8.63 43.94  7.60
42.05  6.27 42.20  4.12
  1   6             155.96
43.06 -7.25 44.00 -8.36 46.00 -8.64 47.71 -8.66 49.34 -8.84 50.70 -7.20
  2  12             153.95
41.06 -1.61 41.35 -3.00 42.25 -4.66 43.23 -6.20 45.00 -6.91 47.35 -7.35
49.42 -6.96 50.91 -5.93 52.10 -4.07 52.95 -3.47 53.26 -2.22 53.31 -1.67
```

```
  3  20             151.90
41.76 -2.87 42.65 -4.45 44.04 -6.13 45.30 -6.69 46.95 -7.09 48.76 -6.77
50.67 -5.95 51.97 -4.76 52.51 -3.69 52.95 -2.36 53.12 -1.30 52.99  -.85
52.37   .69 52.02  3.03 51.77  4.08 42.20  4.12 42.12  3.85 41.91  1.03
41.61  -.24 41.46  -.61
  4  24             149.96
41.84 -3.87 42.55 -5.06 43.68 -6.06 44.78 -6.61 46.47 -6.82 48.02 -6.85
50.00 -6.50 51.37 -5.56 52.04 -4.51 52.64 -3.59 52.76 -3.04 52.64  -.16
52.09   .51 50.80  1.61 49.79  3.19 49.00  4.46 48.38  6.42 46.79  7.79
45.14  7.07 44.28  4.51 43.28  2.07 41.85   .26 41.41  -.72 41.39 -1.11
  5  20             147.96
41.50 -5.40 42.63 -6.15 44.00 -6.74 45.52 -7.31 46.82 -7.39 48.72 -7.05
50.56 -6.56 51.90 -5.85 52.49 -5.22 52.60 -4.66 52.62  -.37 51.83   .99
50.14  2.04 48.45  3.10 46.86  3.39 45.30  3.81 43.35  1.78 41.99   .37
41.41  -.83 41.29 -1.71
  6   9             145.97
52.70  -.53 52.65  -.41 51.48  1.31 50.01  2.14 48.19  2.75 45.85  2.83
43.80  2.11 42.09   .72 41.13  -.53
  7   7             143.93
51.14  1.51 49.85  2.16 48.12  2.36 46.23  2.28 44.64  2.20 43.18  1.55
43.11  1.51
  1  16             145.97
39.73 -6.66 41.11 -7.62 43.10 -8.20 44.71 -8.32 46.47 -8.52 48.12 -8.51
50.60 -7.98 52.61 -7.39 53.61 -6.70 54.07 -6.05 53.95 -3.45 53.42 -2.28
52.70  -.53 41.13  -.53 40.89  -.84 39.87 -2.10
  2  25             143.93
36.44 -7.66 37.97 -8.78 39.98 -9.39 42.54 -9.67 44.70 -9.61 46.27 -9.59
48.41 -9.67 50.96 -9.71 53.08 -9.27 55.49 -8.47 56.75 -7.73 57.25 -6.91
57.25 -6.91 56.74 -4.15 55.98 -3.09 54.45 -1.57 53.09  -.40 51.84  1.16
51.14  1.51 43.11  1.51 41.28   .49 39.58  -.48 37.66 -1.91 36.74 -3.31
36.61 -3.56
  3  34             141.93
33.54 -7.73 34.62 -8.55 36.40-10.10 38.86-10.71 41.41-11.04 43.69-10.90
45.94-10.41 47.04-10.22 49.07-10.52 50.77-10.82 52.69-10.82 54.68-10.57
57.02-10.00 58.76 -9.08 59.23 -8.14 59.96 -7.32 60.36 -6.94 60.03 -3.07
58.90 -2.47 56.44  -.49 55.09   .80 53.26  1.86 51.32  2.77 49.16  3.41
47.17  3.39 45.55  3.52 43.23  3.33 41.20  2.62 38.92  1.24 36.99  -.65
34.91 -2.05 33.69 -2.55 32.22 -3.21 31.40 -3.58
  4  40             139.93
28.36 -6.55 29.03 -8.15 30.51 -8.96 32.29 -9.76 34.49-10.47 36.72-11.49
38.96-11.98 41.60-12.03 43.37-11.71 45.54-11.12 47.36-10.71 49.38-11.24
52.39-11.95 54.91-11.90 56.80-11.56 58.46-11.10 59.61-10.19 61.27 -9.48
63.53 -8.17 65.09 -6.84 65.58 -6.14 65.74 -5.97 65.23 -2.56 63.79  -.77
61.84  -.45 59.74  -.39 57.28   .44 54.86  2.01 51.97  3.76 48.68  4.69
46.43  4.74 43.97  4.66 41.43  3.89 39.52  2.90 37.03  1.13 34.42   .13
32.45  -.21 30.53  -.99 28.93 -2.31 28.36 -3.34
  5  40             137.93
28.96 -8.86 30.00 -9.68 31.98-10.66 34.12-11.38 35.99-12.06 37.72-12.70
39.63-12.93 41.81-12.76 43.62-12.41 45.43-11.54 47.40-11.10 49.69-11.63
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62.72   .61 60.70  1.03 58.82  1.54 56.66  2.34 54.58  3.65 52.20  4.44
50.03  5.28 48.36  5.72 46.18  5.89 42.90  5.68 40.07  4.65 37.92  3.50
36.08  2.28 33.89  1.39 31.52   .53 28.96  -.41
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29.56-10.23 30.16-10.63 32.15-11.66 34.57-12.19 36.28-12.69 38.60-13.73
40.37-13.58 42.64-13.28 44.41-12.65 45.74-11.92 47.19-11.40 48.86-11.89
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61.78-11.33 63.26-10.90 64.73-10.02 64.73   .70 63.07  1.38 61.20  2.26
58.98  3.13 57.13  3.76 54.58  4.92 51.03  6.43 48.69  6.82 45.88  7.01
43.54  6.97 41.11  6.38 38.55  5.18 36.84  4.49 35.25  3.45 33.51  2.46
31.76  1.66 29.69   .71 29.56   .61
  7  37             133.93
30.16-11.45 31.55-12.16 33.36-12.86 35.35-13.04 36.96-13.65 38.22-14.07
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60.81-12.53 62.55-12.10 64.10-11.33 64.10  1.64 62.79  2.65 60.47  3.91
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30.76-12.30 31.42-12.59 33.56-13.16 35.52-13.32 36.89-13.44 38.02-14.29
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61.19-12.76 62.60-12.09 63.64-11.70 63.64  2.88 63.18  3.25 60.98  4.62
59.14  5.48 57.86  7.21 55.20  8.19 52.95  8.47 50.62  8.77 48.51  8.69
46.38  8.59 43.57  8.87 41.15  8.61 38.65  8.24 36.95  7.39 35.87  6.85
32.77  4.22 30.76  2.55
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31.37-12.83 32.77-12.76 35.52-13.23 37.81-14.87 40.81-14.46 42.43-14.38
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46.48 10.73 44.17 11.13 41.12 12.02 37.77 12.07 35.80 11.33 34.03  9.24
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31.76 -3.32 31.84 -4.54
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32.13 -3.91 32.25 -5.28 32.37 -6.66 32.49 -8.03 32.61 -9.41 33.44-10.81
34.53-10.82 35.74-12.25 37.53-13.00 39.34-13.62 41.69-13.94 44.04-13.82
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42.86 12.41 39.23 13.34 36.98 13.43 35.63 12.85 34.11 11.63 32.91  9.57
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32.57 -2.35 32.71 -3.44 32.84 -4.53 32.98 -5.62 33.11 -6.71 34.05 -8.39
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33.91 -3.98 33.91 -4.50 33.91 -5.01 33.91 -5.53 33.91 -6.05 34.33 -7.58
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60.20  -.94 60.14  -.31 60.08   .33 60.02   .96 58.96  2.76 57.61  4.34
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34.25 -3.11 34.27 -3.57 34.29 -4.03 34.30 -4.50 34.32 -4.96 35.56 -7.39
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 10  40            111.92
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40.23  8.70 38.23  6.25 36.20  4.22 34.81  1.58 34.32  -.15
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47.41 11.37 45.03 11.03 42.67 10.40 40.46  9.30 38.73  7.54 37.15  5.66
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58.77  4.30 57.15  5.93 55.61  7.50 53.99  9.07 51.98 10.18 49.78 11.01
47.41 11.37 45.03 11.03 42.67 10.40 40.46  9.30 38.73  7.54 37.15  5.66
35.42  3.70 33.70  1.39 33.55 -1.37
  2  34            107.89
33.81 -3.98 35.52 -6.83 36.91 -8.13 38.33 -8.81 40.13 -9.53 41.89 -9.70
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52.45  9.96 49.72 11.04 46.67 11.35 43.86 10.71 41.27  9.87 39.31  8.29
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32.81 -3.43 34.30 -5.92 36.54 -7.81 39.02 -8.96 41.52 -9.45 43.88 -9.29
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44.90 10.86 42.75 10.46 40.62  9.54 38.81  8.07 37.09  6.40 35.25  4.55
33.34  2.30 32.40  -.51
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32.81 -3.43 34.30 -5.92 36.54 -7.81 39.02 -8.96 41.52 -9.45 43.88 -9.29
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32.20   .17
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62.26  2.54 59.84  5.32 57.52  7.06 54.51  9.69 53.10 10.47 51.11 10.92
49.04 10.95 47.74 10.80 45.95 11.17 43.05 11.15 41.06 10.55 39.57  9.20
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48.30 11.26 47.11 10.70 45.27 11.62 43.02 11.53 41.01 10.70 38.64  9.40
36.00  7.92 34.50  6.15 32.03  4.70 31.53  2.07 30.05  1.12
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29.59 -2.94 30.47 -5.42 32.14 -8.07 33.71 -9.94 35.55-11.97 37.69-13.12
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56.35-14.53 59.00-13.23 60.53-11.89 62.27-10.27 64.01 -7.93 65.16 -5.81
66.03 -3.23 66.12 -2.51 66.29   .89 65.44  2.54 64.20  4.87 61.09  6.98
59.19  7.51 56.99  8.04 53.90  9.35 50.75 10.47 48.43 10.71 45.15 10.78
42.50 10.46 39.30  9.35 35.47  8.32 32.53  6.70 30.21  3.54 29.62  2.06
  9   25          91.80
31.99 -8.19 33.54-10.73 35.67-12.81 38.01-14.22 40.72-14.90 43.15-15.21
45.09-15.36 47.28-15.54 49.72-15.77 52.77-15.94 55.36-15.67 57.77-14.60
59.74-13.30 61.10-12.30 61.10  7.15 60.04  7.57 56.60  8.27 53.04  9.16
48.60  9.74 44.80  9.87 41.93  9.50 38.80  8.73 34.93  7.93 32.92  7.06
31.99  6.46
 10   16          89.90
38.20-14.65 39.31-15.04 42.10-15.43 45.05-15.68 47.16-15.87 49.95-16.19
53.09-16.29 55.67-15.94 55.67  8.09 52.76  8.03 49.36  9.51 46.66  9.63
44.36  9.44 41.90  9.02 39.76  8.36 38.20  8.21
 11    8          87.93
44.30-15.81 44.46-15.82 47.03-15.93 50.10-16.10 50.10  9.15 48.05  9.51
45.20  9.31 44.30  9.16
  1    7         137.93
65.27 -8.52 66.35 -7.26 66.94 -6.34 67.05 -5.92 66.96 -2.74 65.99 -1.16
65.27  -.44
  2    9         135.95
64.73-10.02 64.74-10.02 66.24 -8.86 67.33 -7.36 67.77 -6.40 67.02 -2.37
66.97  -.95 65.17   .52 64.73   .70
  3   11         133.93
64.10-11.33 64.19-11.33 66.31-10.04 67.56 -8.43 68.06 -7.31 68.47 -6.53
68.72 -2.75 67.66  -.92 66.15   .23 64.36  1.51 64.10  1.64
  4   11         131.94
63.64-11.70 64.71-11.29 66.67-10.21 67.80 -9.06 68.51 -7.64 69.00 -6.71
68.87 -2.34 67.87  -.70 66.41   .59 64.71  2.02 63.64  2.88
  5   13         129.94
63.09-11.21 63.90-11.20 65.45-10.90 67.11 -9.82 68.54 -8.26 69.10 -6.85
69.37 -6.11 69.34 -2.51 68.44 -1.09 66.97   .56 65.22  1.28 63.67  1.55
63.09  1.94
  6   23         127.94
62.62 -5.40 62.63 -6.66 62.64 -7.91 62.65 -9.17 62.66-10.42 63.01-10.71
65.22-10.71 66.96-10.00 68.31 -8.68 69.19 -7.19 69.37 -6.36 69.52 -5.98
69.16 -1.87 68.43  -.28 66.97   .82 65.19  1.30 63.53  1.19 62.56   .87
62.56   .87 62.57  -.38 62.58 -1.64 62.59 -2.89 62.60 -4.15
  7   23         125.92
62.44 -5.13 62.30 -6.16 62.31 -7.20 62.25 -8.23 62.18 -9.26 63.33-10.00
64.74-10.36 66.84-10.16 67.47 -9.22 68.06 -7.69 69.42 -6.62 69.65 -5.07
69.47 -1.85 68.50  -.31 67.49   .55 66.01  1.05 64.59  1.15 63.34   .60
62.77   .03 62.70 -1.00 62.64 -2.03 62.57 -3.07 62.51 -4.10
  8   22         123.94
62.11 -4.29 61.90 -5.13 61.85 -5.97 61.72 -6.81 61.59 -7.65 63.37 -9.22
65.01 -9.67 67.11 -9.35 68.50 -8.25 69.43 -6.84 69.92 -5.89 69.85 -1.93
69.25  -.50 67.48   .70 65.59  1.00 64.20   .83 62.95   .19 62.76  -.08
62.63  -.92 62.50 -1.76 62.37 -2.60 62.24 -3.44
  9   22         121.95
61.73 -4.02 61.63 -4.67 61.52 -5.32 61.42 -5.97 61.31 -6.62 62.34 -8.03
63.83 -8.85 65.70 -9.25 67.70 -8.63 69.42 -6.99 70.14 -5.67 70.15 -1.54
69.42   .04 67.74   .96 65.90  1.16 64.17   .61 62.79  -.15 62.26  -.76
62.15 -1.41 62.05 -2.06 61.94 -2.71 61.84 -3.36
 10   25         119.90
61.31 -4.49 61.31 -4.75 61.32 -5.00 61.32 -5.26 61.33 -5.51 61.94 -6.95
62.95 -8.05 64.75 -8.62 66.29 -8.70 68.52 -7.80 69.95 -6.24 70.58 -4.96
70.64 -4.67 70.61 -1.50 69.69   .06 68.07  1.26 66.30  1.23 64.25   .61
62.65  -.60 61.69 -1.92 61.28 -3.22 61.29 -3.47 61.29 -3.73 61.30 -3.98
61.30 -4.24
 11   25         117.91
61.73 -4.31 61.74 -4.52 61.75 -4.72 61.76 -4.93 61.77 -5.13 62.14 -5.90
63.51 -7.52 64.84 -8.00 66.40 -8.14 68.70 -7.37 70.41 -5.86 71.05 -4.47
71.15 -4.10 71.09 -1.12 69.16  1.17 67.14  1.64 65.59  1.05 64.00   .15
62.03  -.96 61.92 -2.44 61.69 -3.29 61.70 -3.49 61.71 -3.70 61.72 -3.90
```

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71.74 -1.37 70.42   .97 68.60  1.68 66.93  1.72 64.95   .98 63.63  -.20
62.62 -1.80 62.40 -2.07 62.40 -3.07 62.40 -3.27 62.40 -3.47 62.40 -3.67
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65.62 -6.78 67.35 -7.13 69.12 -6.63 70.56 -5.77 71.80 -4.74 72.02 -4.26
72.12 -1.80 71.27  0.00 69.74  1.38 68.07  1.77 66.05  1.53 65.02   .73
63.80  -.64 63.15 -2.32 63.09 -2.55 63.09 -2.73 63.08 -2.90 63.08 -3.08
63.07 -3.26
 14  24               111.92
63.69 -2.83 63.68 -3.00 63.66 -3.16 63.65 -3.33 63.64 -3.49 64.53 -5.11
65.78 -6.05 68.47 -6.44 70.23 -6.18 72.11 -5.42 72.80 -4.51 72.85 -2.15
71.99  -.65 70.90   .70 69.36  1.69 67.98  1.09 66.43  1.63 64.81   .18
63.95 -1.35 63.75 -2.01 63.74 -2.17 63.73 -2.34 63.71 -2.50 63.70 -2.67
 15  16               109.92
64.43 -2.94 65.22 -4.48 67.41 -5.80 68.50 -5.77 69.66 -5.77 71.16 -5.93
72.91 -5.72 73.73 -4.68 73.69 -2.22 72.76 -1.22 70.65  1.15 68.15  2.20
66.69  1.84 65.21   .60 64.53 -1.01 64.51 -1.80
 16   9               107.92
64.97 -2.97 65.53 -4.05 65.99 -4.50 71.79   .63 70.25  1.04 68.27  2.40
66.58  1.75 65.42   .16 65.04 -1.49
  1  12               107.92
65.99 -4.50 66.48 -4.97 67.86 -5.10 69.18 -5.19 70.37 -5.14 71.67 -5.60
73.25 -5.76 74.28 -5.16 74.93 -4.54 74.98 -2.05 72.75  -.12 71.79   .63
  2  16               105.90
65.96 -1.71 66.80 -3.44 68.19 -4.66 70.03 -5.33 71.97 -5.75 74.41 -5.81
75.68 -4.52 75.93 -3.99 75.96 -1.86 73.77   .52 72.03  1.55 70.06  2.30
68.22  2.28 66.81  1.53 66.02   .19 65.80  -.27
  3  16               103.90
67.01 -2.40 68.11 -3.66 69.61 -5.20 71.56 -5.75 73.58 -5.98 75.50 -5.45
76.75 -4.06 76.84 -3.57 76.88 -1.80 75.68  -.03 73.90  1.13 72.11  2.05
70.03  2.20 68.23  1.61 66.96  0.00 66.87  -.63
  4  17               101.07
67.95 -2.50 68.67 -3.38 69.64 -4.80 71.07 -5.66 73.12 -5.93 74.83 -5.77
76.25 -5.22 77.22 -4.28 77.34 -3.81 77.42 -1.32 76.38   .17 75.09  1.18
73.37  1.04 71.43  2.01 69.83  1.66 68.26   .28 67.83  -.64
  5  15                99.80
68.95 -2.70 69.85 -4.14 71.14 -5.40 73.07 -5.90 75.09 -5.79 76.86 -5.17
77.95 -3.92 78.07 -3.54 78.02 -1.09 76.86   .60 75.14  1.54 72.86  1.87
70.76  1.54 69.42   .45 68.82  -.54
  6  16                97.80
69.95 -2.87 71.00 -4.17 71.92 -5.20 73.89 -5.71 75.85 -5.67 77.70 -4.84
78.65 -3.64 78.77 -3.23 78.72  -.98 77.51   .52 75.95  1.53 73.99  1.85
72.33  1.54 70.92   .76 69.97  -.52 69.84  -.98
  7  14                95.89
71.07 -2.74 72.84 -3.89 74.08 -5.36 75.75 -5.42 77.84 -5.10 79.00 -3.98
79.49 -3.13 79.53  -.92 78.41   .72 76.29  1.50 74.21  1.63 72.27  1.22
71.13  -.17 70.91  -.93
  8  14                93.94
72.20 -2.51 73.27 -3.72 74.58 -4.49 76.73 -5.04 78.76 -4.56 80.13 -3.59
80.45 -2.89 80.42  -.97 79.17   .44 77.56  1.18 75.72  1.23 74.05  1.09
72.70   .38 72.24  -.73
  9  14                91.89
73.66 -2.76 74.62 -3.80 76.90 -4.53 79.72 -4.28 80.95 -3.49 81.61 -2.62
81.61 -2.62 81.66  -.86 80.65   .43 78.91  1.07 76.79  1.18 74.80   .61
73.78  -.45 73.69  -.96
 10  14                89.92
75.04 -2.34 75.83 -3.46 77.07 -4.10 78.77 -4.17 80.84 -3.86 82.10 -3.11
82.65 -2.38 82.61  -.75 81.71   .30 80.40  1.06 78.62  1.19 76.87   .98
75.52   .06 74.86  -.69
 11  14                87.93
76.20 -1.79 77.15 -2.99 78.63 -3.02 80.39 -3.80 82.09 -3.55 83.43 -2.79
83.73 -2.35 83.70  -.90 83.05  -.01 81.30   .89 79.43  1.42 77.44   .99
76.24  -.02 76.02  -.63
  1  16                85.90
77.90 -2.03 79.12 -3.54 80.80 -3.55 82.32 -3.32 83.63 -2.82 84.34 -2.35
84.89 -1.52 85.15 -1.18 85.46   .05 84.66  1.54 83.48  1.43 82.05  1.31
80.01  1.32 78.56   .72 77.81  -.09 77.61  -.59
  2  15                83.93
79.19 -2.23 80.66 -2.80 82.32 -2.90 84.17 -2.76 85.60 -2.25 87.02 -1.92
88.02 -1.07 88.22   .90 86.75  2.16 84.59  2.40 82.90  2.02 81.93  1.82
80.45  1.61 79.13   .46 78.75  -.88
  3  18                81.93
79.46 -1.03 81.02 -2.09 82.85 -2.59 84.05 -2.59 86.46 -2.37 87.89 -2.11
88.65 -1.35 89.23 -1.12 89.39  -.93 89.42   .59 88.39  1.24 86.74  1.94
85.39  1.92 83.59  1.58 82.31  1.40 80.24  1.50 79.30   .78 79.26   .39
  4  17                79.93
79.86  -.29 81.10 -1.53 82.68 -2.12 84.66 -2.40 86.53 -2.20 88.02 -1.92
88.96  -.05 90.10  -.71 90.41  -.40 90.40   .97 89.28  1.10 88.14   .82
```

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86.40  1.11 84.52  1.02 82.25  1.46 80.29  1.67 79.78   .82
  5  20              77.87
80.73  -.09 82.23 -1.22 83.02 -1.85 85.64 -1.99 87.35 -1.68 88.39 -1.52
89.42  -.58 89.94  -.21 90.65  -.11 90.92   .10 90.95  1.06 89.92  1.07
89.04   .69 88.22   .79 86.73   .81 85.19  1.05 83.12  1.55 81.37  1.77
80.60  1.29 80.58   .89
  6  19              75.89
81.73   .27 82.90  -.10 83.65  -.41 84.54  -.76 85.50 -1.05 86.65 -1.30
87.67  -.81 89.37  -.91 89.80  -.51 89.02   .66 88.09  1.19 87.91   .99
87.30   .75 86.22   .94 85.09  1.15 83.76  1.45 82.40  1.79 81.84  1.54
81.61  1.29
  7  22              73.92
82.85   .96 83.54   .59 84.33   .68 84.91   .00 85.79  0.00 86.40  -.20
87.37  -.72 88.17  -.60 88.62  -.39 89.31  -.55 90.19  -.40 90.31  -.36
90.31  -.36 90.36   .70 89.39  1.21 88.00  1.05 87.20  1.25 86.30  1.32
85.29  1.87 84.40  1.96 83.32  2.13 82.96  1.94
  8  19              71.93
83.94  1.20 84.90  1.12 85.42   .59 86.32   .45 86.99   .42 87.64  -.22
88.89  -.21 89.83  -.41 90.51  -.32 90.63  -.22 90.74   .54 89.81   .96
88.94   .99 88.14  1.37 87.03  1.30 86.34  1.80 85.41  1.76 84.65  2.15
83.92  2.02
  9  14              69.93
86.29  1.14 87.14   .65 87.77   .67 88.65   .00 89.41   .09 90.15  -.19
90.18  -.19 90.30   .65 89.57   .69 88.89  1.20 87.93  1.10 87.09  1.74
86.30  1.64 86.30  1.64
 10   3              67.91
88.59   .40 89.10   .30 88.00   .73
  1   5             139.93
28.32 -6.46 28.36 -6.55 28.36 -3.34 28.25 -3.53 28.14 -4.04
  2   7             137.93
27.31 -7.15 28.70 -8.65 28.96 -8.86 28.96  -.41 28.75  -.49 27.37 -2.37
26.87 -3.16
  3   8             135.95
26.16 -6.88 26.88 -8.41 28.43 -9.49 29.56-10.23 29.56   .61 27.34  -.96
26.57 -2.46 26.09 -3.39
  4  11             133.93
25.64 -7.30 26.10 -8.37 27.68 -9.79 29.65-11.19 30.16-11.45 30.16  1.90
29.09  1.76 27.97   .06 26.76 -1.19 25.72 -2.63 25.44 -3.20
  5  13             131.94
24.99 -6.98 25.71 -8.35 26.98 -9.54 28.38-10.87 30.02-11.90 30.76-12.30
30.76  2.55 30.69  2.49 29.14  1.39 27.26  -.07 25.80 -1.82 25.05 -3.10
25.02 -3.20
  6  13             129.94
24.83 -6.95 25.78 -8.61 27.10-10.49 29.20-11.62 31.25-11.97 31.37-12.03
31.37  2.62 31.13  2.29 30.16   .90 28.15   .78 26.34  -.80 25.02 -2.30
24.75 -3.10
  7  22             127.96
24.74 -7.07 25.87 -8.94 27.15-10.31 28.51-11.10 30.37-11.42 31.56-11.26
32.21-10.71 32.14 -9.50 32.06 -8.20 31.99 -7.07 31.91 -5.85 31.84 -4.64
31.76 -3.42 31.69 -2.21 31.61  -.99 31.54   .22 30.24   .52 28.17   .51
26.62  -.05 25.45 -1.32 24.66 -2.50 24.60 -2.90
  8  24             125.95
24.26 -6.33 24.96 -8.17 26.22 -9.53 27.64-10.28 29.35-10.80 30.76-10.68
32.21-10.15 32.59 -9.49 32.61 -9.41 32.45 -8.37 32.30 -7.32 32.14 -6.28
31.99 -5.23 31.83 -4.19 31.68 -3.14 31.52 -2.10 31.37 -1.05 31.21  -.01
29.37   .45 27.10   .15 25.50 -1.22 24.57 -2.24 24.36 -2.77 24.36 -2.77
  9  22             123.97
24.23 -6.40 25.25 -8.07 26.56 -9.12 28.25-10.05 30.34-10.25 31.43 -9.82
32.69 -8.92 33.08 -8.10 33.09 -7.96 32.81 -7.08 32.54 -6.19 32.26 -5.31
31.99 -4.42 31.71 -3.54 31.44 -2.65 31.16 -1.77 30.89  -.88 30.61  0.00
28.01   .32 26.79   .27 25.09  -.70 24.08 -2.29
 10  24             121.90
23.86 -5.65 24.47 -6.79 25.55 -8.09 27.30 -9.07 29.04 -9.35 30.80 -9.20
32.43 -8.37 33.03 -7.10 33.11 -6.71 32.94 -6.08 32.78 -5.45 32.61 -4.81
32.45 -4.18 32.28 -3.55 32.12 -2.92 31.95 -2.28 31.79 -1.65 31.62 -1.02
29.56   .17 27.46   .46 25.69   .22 24.22  -.92 23.67 -1.99 23.67 -2.16
 11  24             119.91
23.43 -5.25 23.99 -6.20 25.15 -7.44 26.97 -8.39 28.55 -8.55 30.45 -8.13
32.33 -6.87 32.65 -5.61 32.72 -5.06 32.70 -4.77 32.68 -4.47 32.65 -4.18
32.63 -3.88 32.61 -3.59 32.59 -3.29 32.56 -3.00 32.54 -2.70 32.52 -2.41
31.46 -1.24 29.34   .23 26.96   .78 24.83   .37 23.52  -.88 23.25 -1.62
 12  24             117.93
22.79 -4.41 23.67 -6.12 25.09 -7.29 26.80 -7.77 28.51 -7.62 30.12 -7.26
31.72 -5.89 32.16 -4.59 32.17 -4.44 32.18 -4.30 32.19 -4.15 32.20 -4.00
32.20 -3.86 32.21 -3.71 32.22 -3.56 32.23 -3.42 32.24 -3.27 31.68 -2.07
30.59  -.52 29.17   .53 27.10  1.16 25.15  1.02 23.32  -.35 22.76 -1.43
 13  24             115.93
22.40 -4.01 23.64 -6.19 25.13 -7.00 26.70 -7.54 28.44 -7.39 29.99 -6.39
31.15 -5.04 31.36 -3.90 31.37 -3.75 31.38 -3.60 31.30 -3.45 31.39 -3.30
31.40 -3.15 31.41 -3.00 31.41 -2.85 31.42 -2.70 31.43 -2.55 30.74 -1.26
29.69   .25 27.07  1.10 26.07  1.30 24.08   .79 22.36 -1.16 22.16 -1.76
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```

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21.60 -4.84 23.50 -6.41 25.13 -6.89 26.71 -7.00 20.36 -6.73 29.70 -5.65
30.61 -3.70 30.61 -3.31 30.60 -3.10 30.60 -3.04 30.59 -2.91 30.59 -2.77
30.50 -2.64 30.50 -2.50 30.57 -2.37 30.57 -2.23 30.56 -2.10 29.53  -.37
27.42  1.19 25.76  1.45 23.49   .02 22.19  -.51 21.64 -1.61
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20.99 -5.21 22.41 -6.22 24.25 -6.55 26.26 -6.01 20.10 -6.11 29.56 -4.00
29.95 -3.39 29.94 -3.21 29.94 -3.02 29.93 -2.84 29.92 -2.65 29.92 -2.47
29.91 -2.20 29.90 -2.10 29.90 -1.91 29.89 -1.73 29.23  -.32 20.02  1.14
26.61  1.50 24.01  1.50 22.03   .35 21.29 -1.55 20.73 -2.30
 16   14            109.93
23.30 -6.20 24.20 -5.99 25.20 -5.01 27.09 -5.05 20.20 -4.07 20.90 -3.74
29.32 -2.70 20.97  -.75 20.05   .00 25.32  1.06 23.00  1.52 22.14   .01
20.67 -1.49 20.61 -1.55
  1    7            109.93
19.63 -5.05 20.42 -5.05 21.52 -6.46 23.04 -6.29 23.30 -6.20 20.61 -1.55
19.66 -2.62
  2   19            107.91
10.46 -4.99 20.29 -6.15 21.57 -6.14 22.70 -5.09 23.66 -5.61 24.97 -5.40
26.71 -4.99 27.65 -3.09 20.01 -2.90 20.47 -1.97 20.54 -1.42 20.24   .27
27.05  1.32 25.49  1.90 24.21  1.76 22.51  1.00 20.92   .00 19.20 -1.27
10.35 -2.43
  3   16            105.92
17.75 -4.90 19.09 -6.30 21.52 -6.15 23.06 -5.00 24.71 -5.69 26.14 -4.90
27.22 -3.10 27.04 -2.02 27.69   .12 26.44  1.17 24.09  1.63 22.94  1.51
21.06   .07 19.30  -.34 17.66 -1.70 17.49 -2.25
  4   16            103.93
17.04 -4.49 17.58 -5.34 19.44 -6.56 21.61 -6.47 23.72 -5.09 25.65 -4.35
26.90 -2.09 26.96 -2.17 26.75  -.59 25.91   .67 23.63  1.46 22.20  1.25
20.27   .94 10.45  -.25 17.07 -1.52 16.05 -2.04
  5   15            101.90
16.45 -4.61 17.58 -5.66 19.27 -6.50 21.09 -6.47 23.31 -5.91 24.67 -4.06
25.07 -2.99 26.00 -2.20 25.03  -.91 24.69   .43 22.09  1.33 21.02  1.33
19.02   .59 16.94 -1.05 16.44 -1.05
  6   16             99.92
15.94 -4.63 16.03 -5.40 10.10 -6.15 19.54 -6.51 20.90 -6.39 22.56 -5.51
24.10 -4.29 24.75 -3.12 25.01 -2.61 25.15 -1.26 24.25  -.00 22.59   .94
20.60  1.11 10.72   .02 17.06  0.00 15.76 -1.53
  7   15             97.91
15.20 -4.14 16.39 -5.50 10.01 -6.22 19.91 -6.35 21.59 -5.60 22.02 -4.51
23.70 -3.33 23.95 -2.60 23.97 -1.27 22.01   .02 21.06   .73 19.06  1.02
17.10   .30 15.57  -.65 15.01 -1.45
  8   15             95.90
14.67 -4.05 15.25 -5.04 16.96 -5.02 10.69 -5.05 20.66 -5.53 22.03 -4.47
22.66 -3.21 22.05 -2.50 22.07 -1.47 21.50  -.01 19.74   .91 17.32   .57
15.30  -.10 14.52 -1.23 14.52 -1.23
  9   14             93.97
13.93 -3.95 15.21 -5.10 16.99 -5.40 10.60 -5.30 20.42 -4.63 21.32 -3.54
21.50 -2.05 21.66 -1.29 20.66  -.03 10.70   .64 16.59   .59 14.76  -.17
13.76  -.94 13.66 -1.32
 10   14             91.90
12.02 -3.73 13.93 -5.02 15.45 -5.13 17.26 -5.15 19.10 -4.42 19.99 -3.44
20.29 -2.67 20.41 -1.19 19.30   .06 10.10   .57 16.23   .61 14.35   .00
13.09  -.72 12.76 -1.39
 11   14             89.93
11.74 -3.19 12.61 -4.30 14.22 -4.76 15.94 -4.71 17.06 -4.06 10.03 -3.22
19.11 -2.40 19.16 -1.39 10.42  -.36 17.05   .30 15.11   .55 13.70   .20
12.40  -.51 11.76 -1.50
 12   15             87.94
10.67 -3.10 11.45 -3.95 12.06 -4.30 14.49 -4.44 16.13 -4.09 17.32 -3.09
17.67 -2.31 17.04 -2.20 17.92  -.06 16.79   .07 15.23   .42 13.59   .37
12.01  -.29 10.77 -1.24 10.56 -1.66
  1   15             85.93
 9.02 -2.62 11.02 -3.02 12.47 -3.90 14.46 -3.92 15.71 -3.50 16.43 -2.63
16.62 -2.23 16.50 -1.12 15.69  -.22 14.50   .25 13.00   .55 11.50   .57
 9.75   .94  8.04   .41  8.60   .07
  2   16             83.93
 7.19 -1.07  8.60 -3.13 10.45 -3.56 11.06 -3.70 13.50 -3.65 14.96 -3.05
15.50 -2.39 15.05 -1.90 15.02  -.41 14.70   .57 13.52   .77 11.70   .09
10.26  1.57  8.70  1.40  7.54   .76  7.37   .30
  3   10             81.94
 5.71 -1.50  6.21 -2.05  7.04 -3.12  8.55 -3.49 10.35 -3.46 12.22 -3.39
14.02 -2.01 15.12 -1.00 15.47 -1.43 15.57 -1.26 15.30   .04 14.00   .79
12.92   .60 11.57   .50  9.70  1.23  7.94  1.45  6.34   .05  5.90   .44
  4   19             79.93
 5.15 -1.45  5.05 -1.69  6.53 -2.99  7.52 -3.21  8.95 -3.36 10.59 -3.21
12.40 -2.00 13.00 -2.22 14.57 -1.49 14.95  -.99 14.90   .15 13.59   .75
11.00   .46 10.65   .03  9.05   .31  7.57   .27  6.99   .19  5.61   .64
 5.05   .30
  5   20             77.80
 3.93 -1.22  4.00 -1.37  5.60 -1.31  6.10 -2.31  7.17 -2.70  8.90 -3.01
10.49 -2.91 12.19 -2.55 13.03 -1.05 13.06 -1.54 14.39  -.93 14.26   .23
13.40   .70 12.46   .52 10.90   .24  9.24  -.26  7.56  -.12  5.73  -.26
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 4.03   .35  3.94   .21
  6  21            75.90
 5.40 -1.67  6.00 -2.14  7.95 -2.05  9.13 -2.64 10.03 -2.33 10.69 -2.00
11.71 -1.66 12.17 -1.20 12.86 -1.02 13.23  -.65 13.26   .11 12.41   .63
11.60   .39 11.13   .02 10.27  -.27  9.47  -.50  8.37  -.44  7.59  -.70
 6.69  -.12  5.72   .02  5.35  -.18
  7  21            73.92
 5.19 -1.50  6.24 -1.63  7.03 -1.48  7.93 -2.04  8.95 -1.98  9.38 -1.77
10.35 -1.67 11.21 -1.01 12.03  -.78 12.54  -.42 12.63   .37 11.65   .83
10.96   .52 10.41   .20  9.33   .04  8.59  -.11  7.40  -.16  6.79  -.35
 6.01   .16  5.17  0.00  5.03  -.16
  8  17            71.96
 4.91 -1.55  6.02 -1.54  6.65 -1.46  7.57 -1.89  8.53 -1.54  9.15 -1.44
10.20 -1.15 10.71  -.70 11.32  -.60 11.78  -.32 10.29  -.18  9.27  -.06
 8.29  -.33  7.36  -.27  6.34  -.56  5.59  -.31  4.78  -.44
  9  14            69.94
 4.95 -1.44  5.72 -1.40  6.12 -1.52  6.86 -1.87  7.86 -1.67  8.82 -1.63
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 5.06  -.94  5.06  -.94
 10   1            67.91
 6.82 -1.57
  1  10            91.88
61.10-12.30 61.72-11.90 63.02-10.41 64.89 -6.76 66.04 -3.80 66.19 -2.76
65.73  2.09 64.92  4.22 62.12  6.81 61.10  7.15
  2  16            89.90
55.67-15.94 56.13-15.88 59.34-14.15 61.68-12.44 63.38-10.52 64.81 -8.10
65.74 -5.53 66.10 -3.39 66.10 -3.39 65.89  1.71 65.00  3.50 63.40  5.31
61.81  6.72 59.13  7.36 56.23  7.95 55.67  8.09
  3  20            87.93
50.10-16.10 50.81-16.23 54.01-16.38 56.53-16.00 59.19-14.75 61.06-13.45
62.72-11.70 64.69 -9.72 65.99 -6.89 66.65 -4.89 66.84 -4.15 66.45  1.70
65.21  4.10 63.49  6.77 61.67  7.26 59.42  7.45 56.76  7.63 53.35  8.45
50.70  9.06 50.10  9.15
  4  22            85.90
47.45-15.75 48.56-15.80 51.22-16.13 53.64-16.36 56.64-15.88 58.62-15.09
61.01-13.87 63.23-11.10 65.38 -8.96 66.55 -6.29 66.90 -4.59 66.70  1.10
66.09  3.13 64.61  5.21 63.03  6.95 60.86  7.87 58.09  8.09 55.49  7.95
53.39  7.90 51.10  8.54 49.19  9.03 47.45  9.16
  5  23            83.92
47.45-14.77 47.79-14.79 50.14-15.43 52.64-15.95 56.10-15.69 58.80-14.62
60.65-14.03 62.35-12.71 63.67-11.10 65.20 -8.99 66.67 -6.01 67.00 -3.92
66.80  1.49 65.44  3.87 64.24  5.99 62.24  7.40 60.02  8.27 57.00  8.38
54.54  8.10 53.10  7.47 51.49  7.65 49.29  8.27 47.45  8.40
  6  23            81.92
47.45-13.09 49.47-14.22 52.04-15.03 53.80-15.13 56.60-14.73 58.94-14.77
60.92-13.93 63.17-11.84 65.40 -9.04 66.60 -6.92 67.00 -5.41 66.89   .39
66.11  2.22 64.07  4.57 63.70  6.01 61.86  7.56 59.70  8.39 57.11  8.40
54.41  7.93 52.34  7.40 51.19  6.14 49.14  6.71 47.45  6.96
  7  24            79.92
47.45-10.47 47.67-10.44 49.25-12.00 51.52-13.23 53.51-13.49 55.89-14.14
59.03-14.04 61.66-12.68 64.00-10.81 65.64 -9.84 66.55 -7.34 66.93 -5.79
66.77   .82 65.67  2.73 64.20  5.33 62.40  7.00 60.31  8.14 57.94  8.62
55.23  8.26 51.49  6.61 50.13  5.36 49.36  4.25 47.70  4.49 47.45  4.47
  8   1            78.05
47.56  2.24
  1  32            77.84
49.33 -2.00 49.43 -3.96 49.54 -5.13 49.64 -6.29 49.75 -7.46 50.00 -9.03
52.35-11.26 54.65-12.26 56.87-12.83 59.26-12.75 61.70-11.95 64.15-10.45
65.36 -8.93 66.30 -7.14 66.71 -5.99 66.51   .90 65.49  3.07 64.20  5.28
62.00  6.49 60.94  7.99 58.75  8.43 55.87  8.31 53.46  7.60 51.85  6.58
50.20  5.51 49.32  4.09 48.81  3.03 48.80  3.03 48.91  1.86 49.01   .70
49.12  -.47 49.22 -1.63
  2  34            75.89
48.32 -3.00 48.37 -3.77 48.41 -4.54 48.46 -5.31 48.51 -6.08 49.32 -7.92
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63.94-10.16 65.30 -8.60 66.34 -6.81 66.64 -5.72 66.65 -5.72 66.13  1.29
65.15  3.16 64.01  5.00 62.40  6.60 59.95  8.01 57.19  8.32 54.21  7.62
51.90  6.55 50.50  5.25 49.33  3.66 48.50  2.30 48.15  1.34 48.00   .86
48.13   .09 48.10  -.60 48.22 -1.45 48.27 -2.22
  3  32            73.90
48.11 -2.21 48.10 -2.80 48.09 -3.39 48.07 -3.90 48.06 -4.57 48.54 -6.93
49.66 -8.84 51.31-10.23 53.34-11.19 55.41-11.72 57.83-11.85 60.44-11.47
62.21-10.69 63.70 -9.67 65.22 -8.19 66.04 -6.36 66.33 -5.34 65.88  1.10
64.61  3.80 63.14  5.77 61.10  7.32 58.72  8.07 56.24  8.00 53.31  7.14
51.14  5.60 49.92  4.30 48.65  2.11 48.10   .73 48.17   .14 48.15  -.45
48.14 -1.04 48.13 -1.63
  4  34            71.92
48.29 -2.89 48.20 -3.41 48.26 -3.93 48.25 -4.45 48.24 -4.97 48.07 -6.80
49.65 -8.39 51.42-10.15 53.31-11.16 55.43-11.57 58.02-11.71 60.80-11.08
62.59-10.21 64.00 -8.90 65.02 -7.61 65.63 -6.17 65.89 -5.53 65.50  1.73
64.27  3.50 63.24  5.20 61.06  6.86 58.76  7.57 56.10  7.57 53.44  6.65
51.53  5.26 50.27  3.81 49.20  2.15 48.52   .61 48.35  -.20 48.35  -.20
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61.71-10.41 63.55 -8.82 64.85 -7.23 65.27 -5.86 65.27 -5.86 65.28  1.64
64.17  3.51 63.24  4.86 61.84  6.03 59.72  7.03 57.31  7.21 54.37  6.66
52.74  5.66 51.41  4.51 50.32  3.63 49.39  1.91 48.63  -.86 48.56  -.99
48.57 -1.41 48.58 -1.83 48.58 -2.24 48.59 -2.66
  6  28             67.88
49.05 -3.61 49.07 -4.13 49.08 -4.66 49.10 -5.18 49.11 -5.71 50.21 -8.37
51.84-10.30 54.20-11.48 56.53-11.85 59.25-11.52 61.11-10.65 63.01 -9.11
64.07 -7.78 64.66 -6.54 65.20   .73 64.37  2.59 63.10  4.40 61.16  6.23
58.16  6.85 54.81  6.66 51.39  3.73 49.76  1.66 49.11   .02 48.98  -.98
48.99 -1.51 49.01 -2.03 49.02 -2.56 49.04 -3.08
  7  30             65.91
49.15 -3.73 49.15 -4.16 49.15 -4.59 49.16 -5.02 49.16 -5.45 49.88 -7.46
51.12 -9.63 53.24-11.20 56.01-12.02 59.06-11.49 62.58 -9.35 63.79 -7.63
64.43 -6.34 64.30  1.29 63.43  3.06 62.03  4.97 60.45  5.73 58.80  6.10
56.67  6.27 54.42  5.73 52.31  4.43 51.30  3.32 50.42  1.90 49.75   .43
49.21 -1.01 49.13 -1.57 49.13 -2.00 49.14 -2.43 49.14 -2.86 49.14 -3.29
  8  29             63.94
49.48 -3.55 49.48 -4.07 49.47 -4.59 49.47 -5.11 49.47 -5.63 50.84 -8.80
52.36-10.45 54.06-11.30 55.97-11.95 58.31-11.82 61.29-10.66 63.13 -8.56
63.89 -6.92 64.21 -6.02 64.23   .52 63.39  2.34 62.11  3.87 60.59  5.06
58.53  5.61 56.46  5.75 54.65  5.22 52.43  3.96 51.17  2.20 49.99   .80
49.49  -.94 49.49 -1.46 49.49 -1.98 49.48 -2.50 49.48 -3.02
  9  27             61.92
49.69 -3.91 49.73 -4.33 49.77 -4.76 49.80 -5.18 49.84 -5.61 50.62 -7.55
52.11 -9.76 54.16-11.40 56.71-11.89 59.09-11.64 61.68 -9.92 63.32 -7.98
63.88 -6.52 63.74   .88 62.94  1.63 61.27  3.80 59.05  4.90 56.89  5.10
54.56  4.76 51.87  2.91 50.27   .66 49.64 -1.01 49.51 -1.70 49.55 -2.21
49.58 -2.63 49.62 -3.06 49.66 -3.48
 10  27             59.93
49.76 -4.33 49.79 -4.77 49.82 -5.21 49.84 -5.65 49.87 -6.09 51.26 -8.81
52.95-10.57 54.94-11.46 56.99-11.65 59.31-11.41 61.83 -9.81 63.05 -8.19
63.61 -6.95 63.45  -.31 62.67  1.23 61.52  2.85 59.39  3.97 57.16  4.38
54.88  4.20 52.50  2.80 50.80   .84 49.92 -1.11 49.63 -2.14 49.66 -2.58
49.68 -3.02 49.71 -3.46 49.74 -3.90
 11  28             57.90
49.84 -4.70 49.87 -5.10 49.91 -5.51 49.94 -5.91 49.97 -6.32 50.60 -8.00
51.98 -9.79 53.22-10.57 54.90-11.50 56.77-11.47 58.92-11.25 61.02-10.11
62.20 -8.70 63.31 -7.15 63.45 -6.67 63.03 -1.15 62.14   .89 60.38  2.82
57.94  3.62 55.69  3.69 53.32  2.90 51.30   .87 50.15 -1.26 49.68 -2.67
49.71 -3.08 49.74 -3.48 49.78 -3.89 49.81 -4.29
 12  19             55.92
49.98 -6.74 50.77 -8.52 52.00 -9.92 53.53-11.08 55.68-11.39 58.46-11.06
61.33 -9.35 62.69 -7.39 63.13 -6.75 62.93 -2.10 62.12   .13 60.68  1.82
58.43  2.99 56.16  3.19 54.37  2.65 52.06  1.16 50.53  -.73 49.91 -2.17
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 13  20             53.92
50.10 -7.94 50.94 -9.22 52.10-10.32 53.67-11.00 55.23-11.25 57.11-11.12
58.98-10.86 60.75 -9.69 61.95 -8.53 62.86 -7.19 62.94 -6.68 62.65 -2.34
61.98   .11 60.59  1.35 57.91  2.42 55.73  2.63 53.77  1.89 51.64  -.28
50.27 -2.27 49.73 -3.70
 14  21             51.91
50.14 -8.31 50.87 -9.51 52.21-10.65 53.85-11.28 55.67-11.33 57.46-11.06
59.56-10.80 61.26 -9.37 62.28 -8.06 62.94 -6.83 63.00 -6.61 62.60 -3.30
61.99 -1.75 61.01   .22 59.10  1.88 57.03  2.51 55.22  2.26 52.87   .61
51.23 -1.62 50.28 -3.04 49.82 -4.59
 15  21             49.92
50.09 -8.04 50.88 -9.68 52.02-10.77 55.03-11.48 56.50-11.15 58.44-11.40
60.59-10.57 61.84 -8.95 62.55 -7.77 63.10 -6.62 62.81 -4.00 62.09 -2.97
61.18 -1.14 59.72   .95 58.05  1.97 56.59  2.08 54.25  1.19 52.44  -.61
51.51 -2.02 50.65 -3.52 49.96 -4.95
  1  21             47.91
50.54 -8.44 51.62-10.15 53.10-11.22 54.85-11.32 56.12-11.19 57.85-11.66
59.85-11.46 61.27-10.29 62.17 -9.20 62.92 -8.12 63.01 -7.49 62.83 -4.86
61.83 -3.17 60.88 -1.35 58.90   .86 56.92  1.35 55.00   .73 53.04 -1.73
51.65 -3.43 50.85 -4.58 50.39 -5.46
  2  18             45.93
51.20 -8.62 52.16 -9.95 54.60-11.01 56.14-11.32 58.05-11.99 60.05-11.93
62.16-10.57 63.12 -8.63 63.31 -7.99 63.08 -5.76 62.57 -3.93 61.40 -2.23
59.93  -.50 57.63   .35 55.36   .00 53.01 -2.46 51.82 -4.37 51.02 -5.43
  3  19             43.94
51.70 -8.26 52.67 -9.76 54.22-11.23 56.21-12.40 57.91-12.79 59.53-12.62
61.98-11.70 63.28 -9.39 63.39 -8.81 63.17 -5.60 62.57 -4.13 61.21 -2.26
59.33  -.82 57.30  -.67 55.61  -.96 54.03 -2.48 52.62 -4.11 51.77 -5.00
51.49 -5.65
  4  18             41.89
52.31 -8.61 53.19-10.30 54.21-11.63 55.88-12.88 57.74-13.57 59.65-13.41
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60.23 -2.04 58.22 -1.52 56.42 -1.90 54.49 -3.02 52.77 -4.02 52.30 -5.09
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52.71 -9.50 53.37-11.21 54.99-12.81 57.11-14.08 59.86-14.11 62.16-13.22
63.47-11.20 63.96 -9.65 63.95 -6.59 63.30 -4.21 62.27 -2.70 60.73 -1.81
58.68 -2.04 56.52 -2.37 53.04 -4.28 52.40 -6.11 52.46 -6.53
  6  19           37.93
52.68 -9.96 53.60-11.82 54.94-13.41 56.93-14.32 59.19-14.66 61.53-14.44
63.79-12.53 64.39-10.15 64.47 -9.67 64.50 -6.54 63.97 -5.22 62.82 -3.22
61.16 -2.11 59.39 -1.94 58.17 -2.26 55.47 -3.54 53.66 -5.09 52.97 -6.17
52.59 -7.48
  7  20           35.87
52.82-11.01 53.82-12.74 55.28-14.09 56.71-14.81 58.37-15.24 60.13-15.22
62.04-14.55 63.28-13.51 64.15-12.05 64.58-10.74 64.72 -6.65 64.08 -5.29
63.20 -3.51 61.61 -2.47 60.46 -2.14 58.15 -2.46 56.29 -3.26 54.37 -4.76
53.02 -6.83 52.42 -8.19
  8  19           33.93
52.68-10.64 53.39-12.54 54.61-13.83 56.80-14.97 58.91-15.31 60.89-15.09
63.50-13.94 64.57-11.68 64.87-10.98 64.82 -6.84 64.20 -5.17 62.96 -3.64
61.05 -2.53 59.12 -2.62 56.41 -3.59 54.59 -4.92 53.24 -6.75 52.70 -7.76
52.40 -8.52
  9  18           31.92
52.83-11.37 53.71-12.98 55.14-14.30 57.16-15.24 58.70-15.47 61.29-15.09
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60.77 -2.67 59.01 -2.95 56.96 -3.75 54.78 -5.38 53.17 -6.93 52.48 -8.27
 10  18           29.92
52.97-11.10 53.86-12.99 55.21-14.22 57.06-15.00 59.16-15.39 61.75-14.79
63.82-13.22 64.95-11.33 65.00-11.03 64.64 -6.71 63.74 -5.13 62.46 -3.55
60.66 -3.09 58.41 -3.16 56.20 -4.41 54.16 -5.87 53.11 -7.48 52.81 -8.28
 11  16           27.91
53.27-11.17 54.38-13.31 56.02-14.06 57.94-14.86 60.19-14.95 61.97-14.45
63.99-12.79 64.70-11.45 64.41 -6.33 63.65 -4.93 62.19 -3.57 59.96 -3.24
57.37 -4.12 55.50 -5.18 53.29 -7.65 53.11 -8.26
 12  18           25.93
53.61-10.47 54.10-11.78 55.57-13.24 57.56-14.22 59.33-14.70 61.54-14.30
63.61-13.07 64.42-11.55 64.49-11.25 64.41 -7.22 63.99 -6.42 62.88 -4.75
61.33 -3.83 59.37 -3.88 57.06 -4.57 55.14 -5.93 53.85 -7.35 53.61 -7.86
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64.12-11.91 64.51-11.21 64.14 -7.37 63.63 -6.05 62.62 -4.84 61.27 -4.34
59.15 -4.31 56.95 -4.95 55.25 -6.03 54.29 -7.39
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54.48-10.10 55.01-11.56 56.37-12.55 58.09-13.44 59.88-13.88 61.80-13.70
63.72-12.19 64.12-11.26 63.71 -6.95 63.23 -6.06 62.18 -4.95 60.28 -4.57
58.63 -4.67 56.85 -5.57 55.34 -6.63 54.66 -7.80 54.55 -8.03
 15  16           19.89
55.20 -9.99 55.53-11.27 56.82-12.48 58.50-13.21 60.61-13.43 62.57-12.86
63.64-11.44 63.87-10.73 63.59 -7.28 63.12 -6.06 62.04 -4.98 60.52 -4.64
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38.85-14.08 40.75-14.42 42.41-14.55 44.23-14.18 46.02-13.33 47.25-12.98
47.45-13.09 47.45  6.96 46.81  7.06 44.54  6.86 43.15  5.91 41.64  7.23
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32.88 -4.87 31.53 -5.81 30.71 -7.13
 16  14             17.94
31.08-10.87 31.85-12.57 33.51-13.06 35.72-12.98 37.30-12.27 38.35-11.21
38.68-10.05 38.65 -8.00 36.92 -5.58 33.97 -4.60 32.62 -5.00 31.54 -5.96
31.14 -6.56 31.14 -6.56
 17  14             15.95
31.35-10.44 31.93-11.86 33.43-12.62 35.26-12.65 37.33-11.86 38.19-10.41
38.45 -9.77 38.28 -7.67 37.62 -6.33 36.13 -5.23 34.30 -4.64 32.75 -4.92
31.60 -5.83 31.43 -6.41
 18  14             13.99
31.87-10.69 32.25-11.68 34.40-12.61 35.93-12.28 37.21-11.56 37.79-10.70
37.95 -9.94 38.09 -7.39 37.22 -5.89 34.74 -4.38 33.17 -4.57 32.04 -5.46
31.68 -6.12 31.68 -6.34
 19  14             11.98
32.06-10.33 32.70-11.31 33.80-12.15 35.18-12.14 36.39-11.41 36.75-11.22
37.54-10.08 37.76 -7.13 37.08 -5.57 35.16 -4.05 34.00 -4.13 32.80 -4.76
32.01 -5.80 31.77 -6.46
 20  16              9.95
31.67 -9.03 32.27-10.23 33.12-10.97 33.96-12.09 35.30-11.94 36.58-10.95
37.53 -8.91 37.77 -7.77 37.73 -6.84 37.18 -5.15 36.22 -3.87 34.86 -3.50
33.28 -3.84 32.09 -5.27 31.68 -6.23 31.60 -6.71
 21  17              7.96
31.48 -8.84 32.43 -9.94 33.38-10.76 33.97-12.17 35.25-12.11 36.14-10.82
36.91 -9.02 37.59 -7.57 37.88 -6.89 37.91 -5.86 37.31 -4.38 36.08 -3.10
34.26 -2.65 32.62 -3.55 31.72 -5.18 31.31 -6.77 31.20 -7.29
  1  10              5.96
31.51 -8.96 32.48 -9.94 33.51-11.40 34.54-11.96 35.91-11.21 36.67 -9.39
37.41 -7.93 37.63 -7.29 37.74 -4.73 37.46 -3.02 37.05 -1.25 35.94   .11
34.62   .73 33.44   .32 32.57 -1.27 31.85 -3.04 31.66 -4.57 31.57 -5.70
  2  17              3.96
31.40 -8.90 32.26-11.07 33.40-12.02 35.22-12.01 36.41-10.69 37.11 -8.88
37.48 -7.66 37.75 -2.22 37.22  1.48 37.20  4.15 36.37  5.17 34.78  5.18
33.15  3.85 31.78  1.31 31.25 -1.56 30.99 -3.05 30.78 -4.28
  3  24              1.94
31.30 -9.84 31.97-11.29 33.06-12.25 34.51-12.61 35.97-11.78 37.03-10.20
37.42 -8.80 38.54  5.36 38.04  7.39 37.66  8.71 36.63  9.58 35.74  9.02
35.24  7.68 34.96  8.88 33.56  9.72 33.09  8.75 32.39  9.04 31.87  8.53
31.12  7.75 30.49  6.08 29.71  4.99 29.41  3.55 29.41  2.38 29.41  1.68
  4  31              0.00
28.62  3.97 28.64  2.49 28.95  1.42 29.43   .05 29.83 -1.64 30.28 -3.98
30.32 -6.67 30.95 -8.96 31.64-10.97 32.75-12.05 34.68-12.28 36.27-11.55
37.21 -9.76 37.34 -7.88 38.48  3.08 38.09  5.47 38.06  8.86 38.13 10.23
37.47 11.96 35.90 12.23 35.01 11.56 34.45 11.96 33.66 11.76 33.02 11.08
32.34 11.50 31.36 10.56 31.09  9.78 30.02  9.16 29.94  8.05 29.19  7.18
28.56  5.83
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APPENDIX H

SOURCE LISTING OF ALL SUBROUTINES OF PROGRAM IMPED WRITTEN UNDER CONTRACT F33615-78-C-0504

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C   DEFINITION OF VARIABLES IN COMMON AREAS*****************************

C.../AAXES/--VARIABLES USED IN DEFINING ANATOMICAL AXES SYSTEMS.
C   S--THE COMPUTED GLOBAL AXES SYSTEM LOCATION OF EACH ANATOMICAL AXES
C      SYSTEM ORIGIN.
C   DCOS--THE DIRECTION COSINES OF EACH ANATOMICAL AXES SYSTEM WITH RES-
C      PECT TO THE GLOBAL AXES.
C   IDEFPT--LANDMARKS USED TO DEFINE THE ANATOMICAL AXES SYSTEMS OF EACH
C      OF THE NINETEEN ELEMENTARY SEGMENTS.
C   ISAME--RELATES EACH COMBINED SEGMENT TO THE ELEMENTARY SEGMENT THAT
C      IT SHARES ANATOMICAL AXES WITH.
C   IPRMU--USED TO PLACE THE ROWS OF DCOS IN PROPER ORDER AFTER COMPU-
C      TATION.
C   ABCDEF--COORDINATES OF THE LANDMARKS USED IN THE DEFINING THE ANA-
C      TOMICAL AXES SYSTEM BEING COMPUTED.
C   NXYZ--DIRECTION COSINES ANATOMICAL WITH RESPECT TO GLOBAL FOR ONE
C      SEGMENT.
C   DCOSAP--DIRECTION COSINES OF THE SEGMENT ANATOMICAL WITH RESPECT TO
C      SEGMENT PRINCIPAL AXES.

C.../POINTS/--LANDMARK COORDINATES AND ASSOCIATED ITEMS.
C   DUMB--SPACE FILLER FOR VARIABLES NOT USED IN THE FOLLOWING ROUTINES.
C   LMARK--THE COORDINATES OF THE 77 ANTHROPOMETRIC LANDMARKS.
C   ISGMK--A LISTING OF THE LANDMARKS ASSOCIATED WITH EACH SEGMENT TO
C      BE CONVERTED TO PRINCIPAL AND ANATOMICAL COORDINATES FOR TABLES
C      7 AND 18, RESPECTIVELY.
C   NLMRK--INDICIES USED TO ASSOCIATE ELEMENTS OF ISGMK WITH THE PROPER
C      SEGMENT.

C.../NAMES/--DATA USED IN THE PREPARATION OF TABLE HEADINGS.
C   ISUB--THE NUMBER TO BE ASSOCIATED WITH THE SUBJECT BEING PROCESSED.
C   SEGNM--NAMES OF THE 25 BODY SEGMENTS.
C   LMKNM--NAMES OF THE 77 ANTHROPOMETRIC LANDMARKS.
C   AXESTL--NAMES OF 6 AXES SYSTEMS USED AS A PORTION OF THE HEADER OF
C      EACH TABLE.

C.../FORM/--FORMATS USED BY NUMEROUS SUBROUTINES.

C.../EIGEN/--DATA PERTAINING TO SEGMENT PRINCIPAL MOMENTS OF INERTIA
C      AND THEIR DIRECTIONS.
C   TEN--INERTIAL TENSOR FOR EACH SEGMENT WITH RESPECT TO AXES LOCATED
C      AT SEGMENT CENTER OF GRAVITY AND ALIGNED PARALLEL TO GLOBAL AXES.
C   EIGVEC--THE DIRECTIONS OF THE PRINCIPAL MOMENTS OF INERTIA.  THIS
C      ALSO SERVES AS THE DIRECTION COSINES OF THE SEGMENT PRINCIPAL WITH
C      RESPECT TO GLOBAL AXES.
C   EIGR--THE PRINCIPAL MOMENTS OF INERTIAL OF EACH SEGMENT.

C.../1/--SOME INERTIAL PROPERTIES OF EACH SEGMENT.
C   XYZCG--GLOBAL AXES LOCATION OF SEGMENT CENTERS OF GRAVITY.
C   SEGVOL--VOLUME OF EACH SEGMENT.

C.../TRANS/--DATA PERTAINING TO THE CHANGE IN GLOBAL AXES SYSTEMS.
C   XA--X COORDINATE OF NEW GLOBAL AXES ORIGIN WITH RESPECT TO THE OLD
C      GLOBAL AXES.
C   YA--Y COORDINATE OF NEW GLOBAL AXES ORIGIN WITH RESPECT TO THE OLD
C      GLOBAL AXES.
C   COSR--COSINE OF THE ANGLE BETWEEN THE NEW AND OLD GLOBAL AXES SYS-
C      TEMS' X AXES.
```

```
C   SINR--SINE OF THE ANGLE BETWEEN THE NEW AND OLD GLOBAL AXES SYSTEMS'
C     X AXES.

C.../SECTA/
C   DUM1--SPACE FILLER FOR VARIABLES NOT USED IN THE FOLLOWING ROUTINES.
C   NSEGCS--NUMBER OF CROSS SECTIONS PER EACH SEGMENT.
C
C
C***********************************************************************
      BLOCK DATA
      COMMON /AAXES/ S(3,25),DCOS(9,25),IDEFPT(6,19),ISAME(6),
     &               IPRMU(3,19),ABCDEF(18),NXYZ(9),DCOSAP(9,25)
      COMMON /POINTS/ DUM0(11100),LMARK(3,77),ISGMK(183),NLMRK(25)
      COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77),AXESTL(2,6)
      COMMON /FORM/ SEVEN(3),EIGHT(2),FIVE(4),SIX(5)
      COMMON /EIGEN/ TEN(25,3,3),EIGVEC(25,3,3),EIGR(25,3)
      COMMON /1/ XYZCG(25,3),SEGVOL(25)
      COMMON /TRANS/ XA,YA,COSR,SINR
      COMMON /SECTA/ DUM1(600),NSEGCS(20)
      DATA IDEFPT / 37, 38, 36, 37, 38, 34,
     &              41,  2, 44, 77,  2,  2,
     &              44,  2,  7,  2,  7,  7,
     &              49, 50,  7, 49, 50,  7,
     &              53, 54, 55, 53, 54,  8,
     &               4, 10, 12,  4, 12,  4,
     &              20, 22, 16, 20, 16, 16,
     &              30, 24, 28, 24, 28, 26,
     &               3,  9, 11,  3, 11,  3,
     &              19, 21, 15, 19, 15, 15,
     &              29, 23, 27, 23, 27, 25,
     &              57, 59, 61, 59, 57, 57,
     &              57, 59, 61, 59, 57, 57,
     &              63, 69, 67, 69, 63, 63,
     &              71, 73, 32, 75, 32, 71,
     &              56, 58, 60, 58, 56, 56,
     &              56, 58, 60, 58, 56, 56,
     &              62, 68, 66, 68, 62, 62,
     &              70, 72, 31, 74, 31, 70/
      DATA ISAME  /  7, 10, 13, 17,  5,  5/
      DATA IPRMU  /  2, 3, 1,      3, 1, 2,
     &               2, 1, 3,      2, 3, 1,
     &               1, 3, 2,      1, 2, 3,
     &               1, 2, 3,      1, 3, 2,
     &               1, 2, 3,      1, 2, 3,
     &               1, 3, 2,      1, 2, 3,
     &               1, 2, 3,      1, 2, 3,
     &               3, 2, 1,      1, 2, 3,
     &               1, 2, 3,      1, 2, 3,
     &               3, 2, 1/
      DATA AXESTL /6H      ,10H    GLOBAL,6H      ,10H PRINCIPAL,
     &             6H      ,10HSEGMENT PA,6H   TOT,10HAL BODY PA,
     &             6H      ,10HANATOMICAL,6HTOTAL ,10HBODY ANATO/
      DATA NLMRK / 0,  7, 15, 28, 34, 42, 49, 55, 61, 68, 74, 80, 84,
     &            91, 97,103,107,114,120,126,136,146,154,162,183 /
      DATA ISGMK /1,34,36,37,38,39,40, 1, 2,39,40,41,42,43,44, 2, 3, 4,
     &             5, 6, 7,42,43,44,45,46,49,50, 7, 8,49,50,51,52, 8,51,
     &            52,53,54,55,56,57, 4, 6,10,12,14,16,46,10,12,14,16,20,
     &            22,20,22,24,26,28,30, 3, 5, 9,11,13,15,45, 9,11,13,15,
     &            19,21,19,21,23,25,27,29,18,54,55,57,18,54,57,59,61,63,
     &            65,59,61,63,65,67,69,32,67,69,71,73,75,17,53,55,56,17,
     &            53,56,58,60,62,64,58,60,62,64,66,68,31,66,68,70,72,74,
     &            10,12,14,16,20,22,24,26,28,30, 9,11,13,15,19,21,23,25,
```

```
&             27,29,18,54,55,57,59,61,63,65,17,53,55,56,58,60,62,64,
&              2, 3, 4, 5, 6, 7, 8,42,43,44,45,46,49,50,51,52,53,54,
&             55,56,57/
 DATA SEVEN /10H(14X,I2,3X,10H,2A10,3(F7,7H.2,4X))/
 DATA EIGHT /10H(15X,*LAND,8HMARKS*/) /
 DATA FIVE /10H(27X,*SEGM,10HENT CENTER,10HS OF GRAVI,4HTY*)/
 DATA SIX /10H22X,* ORIG,10HIN OF SEGM,10HENT ANATOM,10HICAL AXES*,
&           1H)/
 END
```

```
*    SUBROUTINE HTVSVL CONROLS THE COMPUTATIONS INVOLVED IN PREPARING THE
C      TABLE OF %HEIGHT VERSUS %VOLUME.  PARAMETER GRAPH IS A LOGICAL
C      VARIABLE SPECIFYING IF A GRAPH IS TO BE MADE OF THE RESULTING
C      TABLE.
C
C
       SUBROUTINE HTVSVL (GRAPH)
       DIMENSION Z(20,30),VOLORD(203),ZORD(203)
       LOGICAL GRAPH

       NS= 19
       CALL PREPZ (Z,NS)
       CALL TBLPRP (VOLORD,ZORD,Z,NS)

       CALL WTITLE (15,.FALSE.,1)
       WRITE (6,88)
       TOTVOL = 0.
       DO 100 I=1,201
100       TOTVOL = TOTVOL + VOLORD(I)

       PRTVOL = TOTVOL
       DO 200 I=1,201
          VOLI = VOLORD(I)
          VOLORD(I) = PRTVOL/TOTVOL*100.
200       PRTVOL = PRTVOL - VOLI

       WRITE (6,99) (ZORD(I),(201-I)/2,VOLORD(I), I=1,201,4)
       IF (.NOT.GRAPH) RETURN
       DO 300 I=1,201
300       ZORD(I) =  FLOAT((201 - I)/2)
       CALL PLOT (0.,1.5,-3)
       VOLORD(202) = ZORD(202) = 0.0
       VOLORD(203) = 12.5
       ZORD(203) = 10.
       CALL AXIS (0.,0.,8H% HEIGHT,-8,10.,0.,ZORD(202),ZORD(203))
       CALL AXIS (0.,0.,8H% VOLUME,8,8.,90.,VOLORD(202),VOLORD(203))
       CALL LINE (ZORD,VOLORD,201,1,0,0)
       CALL PLOTE (N)

       RETURN
88     FORMAT (10X,*PERCENT OF VOLUME FROM FLOOR TO SPECIFIED HEIGHTS*/)
99     FORMAT (14X,*HEIGHT*,19X,*% HEIGHT*,16X,*% VOLUME*//
     &        (12X,F8.2,21X,I3,18X,F8.2))
       END
```

```
*     SUBROUTINE TBLPRP DISTRIBUTES THE VOLUME ASSOCIATED WITH EACH CROSS
C       SECTION INTO THE 200 INTERVALS TOTAL HEIGHT IS DIVIDED INTO.
C
C
        SUBROUTINE TBLPRP (VOLORD,ZORD,Z,NS)
        COMMON /SECTA/ DUM1(600),NSEGCS(20),DUM2(600),VOL(20,30)
        DIMENSION VOLORD(201), ZORD(201), Z(20,30)

        VOLORD(1) = VOLORD(201) = ZORD(201) = 0.
        ZORD(1) = ZINC = Z(1,1)
        ZINC = ZINC/200.
        DO 100 I=2,200
           VOLORD(I) = 0.
100        ZORD(I) = ZORD(I-1) - ZINC

        DO 200 I=1,NS
           JSTP = NSEGCS(I)
           DO 200 J=1,JSTP
              ZTOP = Z(I,J)
              ZBOT = Z(I,J+1)
              ZMULT = VOL(I,J)/(ZTOP - ZBOT)

              KUP = INT(201. - ZTOP/ZINC)
              KDWN = 200 - INT(ZBOT/ZINC)
              VOLORD(KUP) = VOLORD(KUP) + (ZTOP - ZORD(KUP+1))*ZMULT
              VOLORD(KDWN) = VOLORD(KDWN) + (ZORD(KDWN) - ZBOT)*ZMULT
              KUP = KUP +1
              KDWN = KDWN -1
              IF (KUP.GE.KDWN) GOTO 200
              ZMULT = ZMULT*ZINC
              DO 190 K=KUP,KDWN
190              VOLORD(K) = VOLORD(K) + ZMULT
200           CONTINUE

        RETURN
        END


C     SUBROUTINE PREPZ PREPARES A TABLE OF Z COORDINATES WHICH SERVE AS
C       TOPS AND BOTTOMS FOR EACH CROSSECTIONAL MASS.
C
C
        SUBROUTINE PREPZ (ZNEW,NS)
        COMMON /SECTA/ ZHT(20,30),NSEGCS(20),Z(20,30)
        DIMENSION ZNEW(20,30)

        DO 100 I=1,NS
           ZNEW(I,1) = Z(I,1) + ZHT(I,1)/2.
           JSTP = NSEGCS(I)
           DO 100 J=1,JSTP
100           ZNEW(I,J+1) = ZNEW(I,J) - ZHT(I,J)

        RETURN
        END
```

```
*    SUBROUTINE ANATOM CONTROLS THE COMPUTATION OF THE ORIGIN AND DIREC-
C      TION COSINES OF THE SEGMENT ANATOMICAL AXES WITH RESPECT TO GLOBAL
C      AXES.
C
C
       SUBROUTINE ANATOM
       EXTERNAL FEQ, GEQ, H1EQ, H2EQ
       REAL LMARK,ABCDEF(3,6),NXY,NYZ,NXZ,G1(3),G2(3),DIFF1(3),DIFF2(3)
       REAL ROTMA(3,3),ROTMAT(3,3)
       COMMON /AAXES/ S(3,25),DCOS(9,25),IDEFPT(6,19),ISAME(6),
     &                IPRMU(3,19),A(3),B(3),C(3),D(3),E(3),F(3),
     &                NXY(3),NYZ(3),NXZ(3)
       COMMON /POINTS/ DUM(11100),LMARK(3,77)
       EQUIVALENCE (ABCDEF,A)
       LOGICAL NOROT
       DATA ROTMA/ .86602540, .41413669,-.28016210,
     &            -.28016210, .86602540, .41413669,
     &             .41413669,-.28016210, .86602540/
       CALL TRNSP (ROTMA,ROTMAT)

C    I INCREMENTS THROUGH THE 19 ELEMENTARY SEGMENTS.
       DO 500 I=1,19
C
C    ABCDEF IS FILLED WITH THE COORDINATES OF THE LANDMARKS USED TO
C      DEFINE SEGMENT I'S ANATOMICAL AXES SYSTEM.
          DO 100 K=1,6
             DO 100 J=1,3
100             ABCDEF(J,K) = LMARK(J,IDEFPT(K,I))
          DO 200 J=1,3
             DIFF1(J) = A(J) - C(J)
200          DIFF2(J) = B(J) - C(J)
          CALL CROSS (DIFF1,DIFF2,NXY)
          CALL NORM (NXY)
C
C    IF ANY COMPONENT OF NXY IS > .99 THEN THE COORDINATES OF ABCDEF ARE
C      ROTATATED IN ORDER TO AVOID ZEROS OCCURRING IN THE DENOMINATORS OF
C      SOME EQUATIONS.
          NOROT = AMAX1 (ABS(NXY(1)), ABS(NXY(2)), ABS(NXY(3)))  .LT. .99
          IF (NOROT) GOTO 290
             CALL MATMUL (ROTMA,ABCDEF,ABCDEF,6)
             DO 210 J=1,3
                DIFF1(J) = A(J) - C(J)
210             DIFF2(J) = B(J) - C(J)
             CALL CROSS (DIFF1,DIFF2,NXY)
             CALL NORM (NXY)
290       CALL EVAL (NYZ,GEQ,FEQ,1.)
          CALL NORM (NYZ)
          CALL EVAL (G1,H1EQ,H2EQ,0.)
          CALL EVAL (G2,H1EQ,H2EQ,1.)
          DO 300 J=1,3
             DIFF1(J) = F(J) - G1(J)
300          DIFF2(J) = G2(J) - G1(J)
          T0 = DOT(DIFF1,DIFF2) / DOT(DIFF2,DIFF2)
          DO 400 J=1,3
400          S(J,I) = G1(J) + T0*DIFF2(J)
          CALL CROSS (NXY,NYZ,NXZ)
          CALL NORM (NXZ)
          IF (NOROT) GOTO 500
             CALL MATMUL (ROTMAT,S(1,I),S(1,I),1)
             CALL MATMUL (ROTMAT,NXY,NXY,3)
500       CALL DIREC (I)
```

```
      DO 700 J=20,25
         DO 600 I=1,3
600         S(I,J) = S(I,ISAME(J - 19))
         DO 700 I=1,9
700         DCOS(I,J) = DCOS(I,ISAME(J - 19))

      RETURN
      END



C   SUBROUTINE DIREC IS CALLED BY ANATOM TO PLACE THE ROWS OF DCOS IN
C     THE CORRECT ORDER AS SPECIFIED BY IPRMU.
C
C
      SUBROUTINE DIREC (K)
      REAL NXYZ
      COMMON /AAXES/ S(75),DCOS(3,3,25),DUM0(120),IPRMU(3,19),
     &               DUM1(18),NXYZ(3,3)

      DO 100 J=1,3
         DO 100 I=1,3
100         DCOS(J,I,K) = NXYZ(I,IPRMU(J,K))

      DO 200 I=1,3
         IF (DCOS(I,I,K) .GT. 0.) GOTO 200
            DO 250 J=1,3
250            DCOS(I,J,K) = -DCOS(I,J,K)
200      CONTINUE
      RETURN
      END
```

```
*    SUBROUTINE EVAL IS CALLED BY ANATOM TO COMPUTE A 3-TUPLE OF THE FORM
C      (F(G(Z),Z), G(Z), Z) WERE Z IS SPECIFIED.
C
C
       SUBROUTINE EVAL (PT,EQ1,EQ2,Z)
       REAL PT(3)

       PT(2) = EQ2(Z,DUM)
       PT(1) = EQ1(Z,PT(2))
       PT(3) = Z
       RETURN
       END



C    FUNCTION EQU IS USED BY EVAL TO SUPPLY EQUATIONS NEEDED IN THE COMP-
C      UTATION OF ANATOMICAL AXES SYSTEM ORIGINS.
C
C
       FUNCTION EQU (Z,Y)
       COMMON /AAXES/ DUM(477),A(3),B(3),C(3),D(3),E(3),F(3),
     &                NXY(3),NYZ(3),NXZ(3)
       REAL NXY,NYZ,NXZ

       ENTRY FEQ
       EQU = Z* (NXY(3)*(D(1)-E(1)) + NXY(1)*(E(3)-D(3))) /
     &          (NXY(2)*(E(1)-D(1)) + NXY(1)*(D(2)-E(2)))
       RETURN

       ENTRY GEQ
       EQU = -(Y*NXY(2) + Z*NXY(3))/NXY(1)
       RETURN

       ENTRY H1EQ
       EQU = (DOT(C,NXY) - NXY(2)*Y - NXY(3)*Z)/NXY(1)
       RETURN

       ENTRY H2EQ
       EQU = (DOT(C,NXY) - NXY(1)/NYZ(1)*DOT(D,NYZ) -
     &        Z*(NXY(3) - NXY(1)*NYZ(3)/NYZ(1))) /
     &       (NXY(2) - NXY(1)*NYZ(2)/NYZ(1))
       RETURN
       END
```

```
*    FUNCTION DOT RETURNS THE DOT PRODUCT OF THE TWO THREE DIMENSIONAL
C      VECTORS A AND B.
C
C
      FUNCTION DOT (A,B)
      REAL A(3),B(3)
      DOT = 0.
      DO 100 I=1,3
100      DOT = DOT + A(I)*B(I)
      RETURN
      END



C    SUBROUTINE CROSS COMPUTES THE CROSS PRODUCT OF PARAMETERS A AND B
C      AND RETURNS THE RESULT IN PARAMETER C.
C
C
      SUBROUTINE CROSS (A,B,C)
      DIMENSION A(3),B(3),C(3)

      C(1) = A(2)*B(3) - A(3)*B(2)
      C(2) = B(1)*A(3) - B(3)*A(1)
      C(3) = A(1)*B(2) - A(2)*B(1)
      RETURN
      END



C    SUBROUTINE NORM NORMALIZES THE THREE DIMENSIONAL VECTOR C.
C
C
      SUBROUTINE NORM (C)
      REAL C(3)

      SIZE = 0.
      DO 50 I=1,3
50       SIZE = SIZE + C(I)**2
      SIZE = SQRT(SIZE)
      DO 100 I=1,3
100      C(I) = C(I)/SIZE
      RETURN
      END
```

```
*   SUBROUTINE WTBL56 IS USED TO WRITE OUT TABLES 5 AND 6.
C
C
      SUBROUTINE WTBL56
      COMMON /AAXES/ S(3,25),DCOS(9,25)

      CALL WTITLE (5,.FALSE.,1)
      WRITE (6,99)
      DO 100 I=1,25
100      CALL TBLCOR (S(1,I),I)

      CALL WTITLE (6,.FALSE.,1)
      WRITE (6,88)
      DO 200 I=1,13
200      CALL TBLCOS (DCOS(1,I),I)
      CALL WTITLE (6,.TRUE.,1)
      WRITE (6,88)
      DO 300 I=14,25
300      CALL TBLCOS (DCOS(1,I),I)

      RETURN
88    FORMAT (10X,*DIRECTION COSINES (ANGLES) OF SEGMENT ANATOMICAL*,
     &        * AXES*/30X,*WITH RESPECT TO GLOBAL AXES*/34X,
     &         *(RA) = [DAG] (RG)*/14X,*SEGMENTS*/)
99    FORMAT (33X,*ORIGIN OF SEGMENT ANATOMICAL AXES*/36X,
     &         *WITH RESPECT TO GLOBAL AXES*//14X,*SEG*,16X,*X*,13X,
     &         *Y*,13X,*Z*/)
      END


C   SUBROUTINE WTITLE IS CALLED BY VARIOUS ROUTINES TO WRITE OUT TABLE
C     TITLES.
C
C
      SUBROUTINE WTITLE (ITABLE,CONT,IAXES)
      COMMON /NAMES/ ISUB,DUM(179),AXESTL(2,6)
      DIMENSION CONTIN(2)
      LOGICAL CONT

      CONTIN(1) = CONTIN(2) = 10H
      IF (.NOT.CONT) GOTO 10
      CONTIN(1) = 10H(CONTINUED
      CONTIN(2) = 10H)
10    WRITE (6,99) ITABLE,CONTIN,ISUB,(AXESTL(II,IAXES),II=1,2)

      RETURN
99    FORMAT (*1*//14X,*TABLE #*,I3,1X,A10,A4,*SUBJECT*,I3,3X,A6,A10,
     &         * AXES*//)
      END
```

```
*    SUBROUTINE TBLCOS IS CALLED TO WRITE OUT A TABLE ENTRY CONSISTING
C      OF COSINES ALONG WITH THE CORRESPONDING ANGLE.  TABLES THAT
C      UTILIZE THIS SUBROUTINE IN PRINTING ARE 4,6,13.
C
C
       SUBROUTINE TBLCOS (DCOS,ISEG)
       REAL DCOS(3,3),ANGLE(3),NAME
       COMMON /NAMES/ ISUB,SEGNM(25)

       IF (ISEG.EQ.25) WRITE (6,88)
       NAME = SEGNM(ISEG)
       DO 100 I=1,3
          DO 30 J=1,3
30           ANGLE(J) = ACOS(DCOS(I,J))*57.29578
          WRITE (6,99) NAME,(DCOS(I,J),ANGLE(J),J=1,3)
          NAME = 10H
100       CONTINUE
       WRITE (6,99)

       RETURN
88     FORMAT (/14X,*TOTAL BODY*/)
99     FORMAT (14X,A8,3(F10.5,*(*,F5.1,*)*))
       END


C    SUBROUTINE TBLCOR IS CALLED TO WRITE OUT AN ENTRY IN A TABLE OF
C      COORDINATES.  THIS SUBROUTINE IS UTILIZED IN THE PRINTING OF
C      TABLES 5,8,9,11,12.
C
C
       SUBROUTINE TBLCOR (XYZ,I)
       COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
       REAL XYZ(3)

       IF (2*(I/2) .EQ. I) GOTO 10
       IF (I.EQ.25) WRITE (6,88)
       WRITE (6,99)
10     WRITE (6,99) SEGNM(I),XYZ

       RETURN
88     FORMAT (//14X,*TOTAL BODY*)
99     FORMAT (14X,A8,3(F13.2,2X))
       END
```

```
*   SUBROUTINE TBL7 IS USED TO CONTROL THE WRITING OUT OF TABLE 7.
C
C
      SUBROUTINE TBL7
      COMMON /EIGEN/ DUM0(225),EIGVEC(25,3,3)
      COMMON /1/ XYZCG(25,3)
      COMMON /POINTS/ DUM1(11100),LMARK(3,77)
      COMMON /AAXES/ S(3,25)
      COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
      COMMON /FORM/ SEVEN(3),EIGHT(2)
      LOGICAL CONT
      REAL LMARK,ORGTL(3),CMG(3),DCOS(3,3),XP(3)

      ORGTL(1) = 10HANATOMICAL
      ORGTL(2) = 10H SYSTEM OR
      ORGTL(3) = 10HIGIN
      CONT = .FALSE.

      DO 100 I=1,21,2
         CALL WTITLE (7,CONT,3)
         CONT = .TRUE.
         WRITE (6,99)
         ISTP = I +1
         DO 100 II=I,ISTP
            DO 50 J=1,3
               CMG(J) = XYZCG(II,J)
               DO 50 K=1,3
50                DCOS(K,J) = EIGVEC(II,K,J)
100         CALL RTMRKS (CMG,DCOS,II,S(1,II),ORGTL)

      DO 200 II=23,24
         CALL WTITLE (7,CONT,3)
         WRITE (6,99)
         DO 150 J=1,3
            CMG(J) = XYZCG(II,J)
            DO 150 K=1,3
150            DCOS(K,J) = EIGVEC(II,K,J)
200      CALL RTMRKS (CMG,DCOS,II,S(1,II),ORGTL)

      CALL WTITLE (7,CONT,3)
      WRITE (6,99)
      DO 250 J=1,3
      CMG(J) = XYZCG(25,J)
      DO 250 K=1,3
250   DCOS(K,J) = EIGVEC(25,K,J)
      CALL DEFPT (CMG,DCOS,25)
      WRITE (6,EIGHT)
      DO 300 II=1,34
         CALL CNVRT (LMARK(1,II),XP,CMG,DCOS)
300      WRITE (6,SEVEN) II,(LMKNM(I,II),I=1,2),XP
      CALL WTITLE(7,CONT,3)
      WRITE (6,99)
      DO 350 II=35,77
         CALL CNVRT (LMARK(1,II),XP,CMG,DCOS)
350      WRITE (6,SEVEN) II,(LMKNM(I,II),I=1,2),XP
      CALL OTAXES (CMG,DCOS,25,S(1,25),ORGTL)

      RETURN
99    FORMAT (19X,*SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN*/
     &        26X,*WITH RESPECT TO SEGMENT PA AXES*//15X,*#*,27X,
     &        *X*,18X,*Y*,18X,*Z*/)
      END
```

```
*    SUBROUTINE TBL10 IS USED TO CONTROL THE WRITING OUT OF TABLE 10.
C
C
      SUBROUTINE TBL10
      COMMON /1/XYZCG(25,3)
      COMMON /POINTS/ DUM1(11100),LMARK(3,77)
      COMMON /AAXES/ S(3,25),DCOS(9,25)
      COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
      COMMON /FORM/ SEVEN(3),EIGHT(2)
      LOGICAL CONT
      REAL LMARK,ORGTL(3),CMG(3),XP(3)

      ORGTL(1) = 10HCENTER OF
      ORGTL(2) = 10HGRAVITY
      ORGTL(3) = 10H
      CONT = .FALSE.

      DO 100 I=1,21,2
      CALL WTITLE (10,CONT,5)
         CONT = .TRUE.
         WRITE (6,99)
         ISTP = I +1
         DO 100 II=I,ISTP
            DO 50 J=1,3
50             CMG(J) = XYZCG(II,J)
100         CALL RTMRKS (S(1,II),DCOS(1,II),II,CMG,ORGTL)

      DO 200 II=23,24
         CALL WTITLE (10,CONT,5)
         WRITE (6,99)
         DO 150 J=1,3
150         CMG(J) = XYZCG(II,J)
200      CALL RTMRKS (S(1,II),DCOS(1,II),II,CMG,ORGTL)

      CALL WTITLE (10,CONT,5)
      WRITE (6,99)
      CALL DEFPT (S(1,25),DCOS(1,25),25)
      WRITE (6,EIGHT)
      DO 300 II=1,34
         CALL CNVRT (LMARK(1,II),XP,S(1,25),DCOS(1,25))
300      WRITE (6,SEVEN) II,(LMKNM(I,II),I=1,2),XP
      CALL WTITLE (10,CONT,5)
      WRITE (6,99)
      DO 350 II=35,77
         CALL CNVRT (LMARK(1,II),XP,S(1,25),DCOS(1,25))
350      WRITE (6,SEVEN) II,(LMKNM(I,II),I=1,2),XP
      DO 400 J=1,3
400      CMG(J) = XYZCG(25,J)
      CALL OTAXES (S(1,25),DCOS(1,25),25,CMG,ORGTL)

      RETURN
99    FORMAT (24X,*SEGMENT LANDMARKS AND CENTER OF GRAVITY*/
     &        27X,*WITH RESPECT TO ANATOMICAL AXES*//15X,*#*,27X,
     &        *X*,10X,*Y*,10X,*Z*/)
      END
```

```
*    SUBROUTINE RTMRKS IS CALLED BY TBL7 AND TBL10 TO WRITE OUT THE COM-
C      PONENTS OF LANDMARKS SPECIFIED BY ISGMK FOR SEGMENT II CONVERTED
C      TO THE AXES SYSTEM SPECIFIED BY PARAMETERS S AND DCOS.
C
C
       SUBROUTINE RTMRKS (S,DCOS,II,CM,ORGTL)
       REAL S(3),DCOS(3,3),CM(3),ORGTL(3),XP(3),LMARK
       COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
       COMMON /FORM/ SEVEN(3),EIGHT(2)
       COMMON /POINTS/ DUM(11100),LMARK(3,77),ISGMK(103),NLMRK(25)

       CALL DEFPT (S,DCOS,II)
       WRITE (6,EIGHT)
       JSTP = NLMRK(II+1) - NLMRK(II)
       DO 50 J=1,JSTP
          IMRK = ISGMK(J + NLMRK(II))
          CALL CNVRT (LMARK(1,IMRK),XP,S,DCOS)
50        WRITE (6,SEVEN) IMRK,(LMKNM(I,IMRK),I=1,2),XP

C    ENTRY OTAXES CONVERTS THE PARAMETER CM TO THE AXES SYSTEM SPECIFIED
C      BY S AND DCOS AND WRITES THESE COORDINATES OUT.
C
       ENTRY OTAXES
       WRITE (6,77) ORGTL
       CALL CNVRT (CM,XP,S,DCOS)
       BLANK = 10H
       WRITE (6,SEVEN) 0,BLANK,BLANK,XP
       WRITE (6,SEVEN)

       RETURN
77     FORMAT (/15X,3A10)
       END



C    SUBROUTINE DEFPT IS CALLED BY RTMKS TO CONVERT THE ANATOMICAL AXES
C      SYSTEM DEFINITION POINTS TO THE AXES SYSTEM SPECIFIED BY S AND
C      DCOS AND WRITE THESE COORDINATES OUT.
C
C
       SUBROUTINE DEFPT (S,DCOS,ISEG)
       REAL S(3),DCOS(3,3),XP(3),LMARK
       COMMON /AAXES/ DUM0(300),IDEFPT(6,19),ISAME(6)
       COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
       COMMON /POINTS/ DUM1(11100),LMARK(3,77)
       COMMON /FORM/ SEVEN(3)

       II = ISEG
       IF (II.GT.19)  II = ISAME(II-19)
       WRITE (6,99) SEGNM(ISEG)
       DO 100 I=1,6
          IMRK = IDEFPT(I,II)
          CALL CNVRT (LMARK(1,IMRK),XP,S,DCOS)
100       WRITE (6,SEVEN) IMRK,(LMKNM(J,IMRK),J=1,2),XP
       WRITE (6,SEVEN)

       RETURN
99     FORMAT (15X,*AXES DEFINITION POINTS*,19X,*SEGMENT *,A8/)
       END
```

```
*     SUBROUTINE TOMOUT WRITES CERTAIN PORTIONS OF THE DATA OUT TO A DIF-
C       FERENT FILE THAN USED FOR THE TABLES.  THIS DATA IS IN A FORM MORE
C       EASILY READ BY A COMPUTER PROGRAM THAN THE TABLES.
C
C
        SUBROUTINE TOMOUT
        COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
        COMMON /1/ XYZCG(25,3),SEGVOL(25)
        COMMON /EIGEN/ TEN(25,3,3),EIGVEC(25,3,3),EIGR(25,3)
        COMMON /AAXES/ S(3,25),DCOS(9,25)
        COMMON /POINTS/ DUM(11100),LMARK(3,77)
        REAL LMARK

        WRITE (7,11) ISUB
        WRITE (7,999)
        WRITE (7,99) (I,SEGNM(I),SEGVOL(I),(EIGR(I,J),J=1,3),I=1,25)
        WRITE (7,888)
        WRITE (7,88) (I,(XYZCG(I,J),J=1,3),(S(J,I),J=1,3),I=1,25)
        WRITE (7,777)  10HPRINCIPAL
        WRITE (7,77) (I,((EIGVEC(I,J,K),J=1,3),K=1,3),I=1,25)
        WRITE (7,777) 10HANATOMICAL
        WRITE (7,77) (I,(DCOS(J,I),J=1,9),I=1,25)
        WRITE (7,666)
        WRITE (7,66) (I,(LMKNM(J,I),J=1,2),(LMARK(J,I),J=1,3),I=1,77)
11      FORMAT (*1*,30X,*DATA FOR FEMALE SUBJECT*,I3)
66      FORMAT (I9,6X,2A10,3F10.3)
77      FORMAT (I5,3X,9F8.6)
88      FORMAT (I9,6X,6F10.3)
99      FORMAT (I9,6X,A10,4E12.7)
666     FORMAT (4X,*LANDMARK*,6X,*NAME*,20X,*GLOBAL COORDINATES*)
777     FORMAT (* SEGMENT*,9X,*DIRECTION COSINES *,A10,* W.R.T. GLOBAL *,
      &         *(BY COLUMNS)*)
888     FORMAT (4X,*SEGMENT*,5X,*PRINCIPAL AXES ORIGIN (C.G.)*,5X,
      &         *ANATOMICAL AXES ORIGIN*)
999     FORMAT (4X,*SEGMENT*,7X,*NAME*,6X,*VOLUME*,13X,
      &         *PRINCIPAL MOMENTS*)
        END
```

```
*     SUBROUTINE CNVRT CONVERTS THE COORDINATES OF PARAMETER X TO THE AXES
C       SYSTEM SPECIFIED BY S AND DCOS, PLACING THE RESULTING COORDINATES
C       IN PARAMETER XP.
C
C
      SUBROUTINE CNVRT (X,XP,S,DCOS)
      DIMENSION X(3),XP(3),S(3),DCOS(3,3)

      DO 100 I=1,3
100      XP(I) = X(I) - S(I)
      CALL MATMUL (DCOS,XP,XP,1)
      RETURN
      END



C     SUBROUTINE MATMUL COMPUTES THE MATRIX PRODUCT OF PARAMETERS A AND B
C       AND PLACES THE RESULT IN PARAMETER C.  B AND C MAY BE IDENTICAL IN
C       THE CALLING ROUTINE.
C
C
      SUBROUTINE MATMUL (A,B,C,NCOL)
      DIMENSION A(3,3),B(3,NCOL),C(3,NCOL),ENTRY(3)

      DO 100 J=1,NCOL
         DO 90 I=1,3
            ENTRY(I) = 0.
            DO 90 K=1,3
90             ENTRY(I) = ENTRY(I) + A(I,K)*B(K,J)
         DO 100 K=1,3
100         C(K,J) = ENTRY(K)
      RETURN
      END



C     SUBROUTINE TRNSP COMPUTES THE TRANSPOSE OF PARAMTER A AND PLACES
C       IT IN PARAMETER AT.
C
C
      SUBROUTINE TRNSP (A,AT)
      REAL A(3,3),AT(3,3)

      DO 100 I=1,3
      DO 100 J=1,3
100      AT(J,I) = A(I,J)
      RETURN
      END
```

```
*   SUBROUTINE TBL89 IS CALLED TO WRITE OUT TABLES 8 AND 9.
C
C
      SUBROUTINE TBL89
      COMMON /FORM/ DUM(5),FIVE(4),SIX(5)
      COMMON /AAXES/ S(3,25)
      COMMON /EIGEN/ DUM8(225),EIGVEC(25,3,3)
      COMMON /1/ XYZCG(25,3)
      REAL XP(3),DCOS(3,3),CGT(3),CGS(3)

      CALL WTITLE (8,.FALSE.,4)
      WRITE (6,FIVE)
      WRITE (6,99)
      DO 10 I=1,3
         CGT(I) = XYZCG(25,I)
         DO 10 J=1,3
10          DCOS(I,J) = EIGVEC(25,I,J)

      DO 100 ISEG=1,25
         DO 110 I=1,3
110         CGS(I) = XYZCG(ISEG,I)
         CALL CNVRT (CGS,XP,CGT,DCOS)
100      CALL TBLCOR (XP,ISEG)

      CALL WTITLE (9,.FALSE.,4)
      WRITE (6,SIX)
      WRITE (6,99)
      DO 200 ISEG=1,25
         CALL CNVRT (S(1,ISEG),XP,CGT,DCOS)
200      CALL TBLCOR (XP,ISEG)

      RETURN
99    FORMAT (23X,*WITH RESPECT TO TOTAL BODY PA AXES*//
     &         14X,*SEG*,16X,*X*,13X,*Y*,13X,*Z*/)
      END
```

```
*    SUBROUTINE TBL112 IS CALLED TO WRITE OUT TABLES 11 AND 12.
C
C
      SUBROUTINE TBL112
      COMMON /AAXES/ S(3,25),DCOS(9,25)
      COMMON /1/ XYZCG(25,3)
      COMMON /FORM/ DUMB(5),FIVE(4),SIX(5)
      REAL XP(3),CM(3)

      CALL WTITLE (11,.FALSE.,6)
      WRITE (6,FIVE)
      WRITE (6,99)
      DO 100 ISEG=1,25
         DO 90 J=1,3
90          CM(J) = XYZCG(ISEG,J)
         CALL CNVRT (CM,XP,S(1,25),DCOS(1,25))
100      CALL TBLCOR (XP,ISEG)

      CALL WTITLE (12,.FALSE.,6)
      WRITE (6,SIX)
      WRITE (6,99)
      DO 200 ISEG=1,25
         CALL CNVRT (S(1,ISEG),XP,S(1,25),DCOS(1,25))
200      CALL TBLCOR (XP,ISEG)

      RETURN
99    FORMAT (19X,*WITH RESPECT TO TOTAL BODY ANATOMICAL AXES*//
     &        14X,*SEG*,16X,*X*,13X,*Y*,13X,*Z*/)
      END
```

```
*     SUBROUTINE RWTBL1 READS IN THE HEADER OFF THE DATA SET, PLACING
C       ITEMS IN APPROPRIATE COMMON AREAS.  IT ALSO COMPUTES THE TRANS-
C       FORMATION TO THE ALTERED GLOBAL AXES SYSTEM.  THIS INFORMATION IS
C       APPLIED TO THE LANDMARK COORDINATES AND STORED TO LATER BE APPLIED
C       CROSS SECTION COORDINATES.  ADDITIONALLY THIS SUBROUTINE WRITES
C       OUT TABLE 1.
C
C
        SUBROUTINE RWTBL1
        COMMON /POINTS/ DUM(11100),LMARK(3,77)
        COMMON /NAMES/ ISUB,SEGNM(25),LMKNM(2,77)
        COMMON /FORM/ SEVEN(3)
        COMMON /SECTA/ DUM1(600),NSEGCS(20)
        COMMON /TRANS/ XA,YA,COSR,SINR
        REAL LMARK
        DATA (SEGNM(J),J=20,25) /10HR FARM+H  ,10HL FARM+H  ,
       &     10HR THIGH   ,10HL THIGH   ,10HTORSO     ,10HTOT BODY  /

        READ (9,77) ISUB
        READ (9,88) (SEGNM(J),NSEGCS(J),J=1,19)
        DO 100 IMRK=1,76
100        READ (9,99) (LMKNM(J,IMRK),J=1,2),(LMARK(J,IMRK),J=1,3)
        XA = (LMARK(1,54) + LMARK(1,53))/2.
        YA = (LMARK(2,54) + LMARK(2,53))/2.
        DELX = LMARK(1,54) - LMARK(1,53)
        DELY = LMARK(2,53) - LMARK(2,54)
        DASIS = SQRT(DELX**2 + DELY**2)
        COSR = DELY/DASIS
        SINR = DELX/DASIS
        DO 150 IMRK=1,76
150        CALL FTOM (LMARK(1,IMRK),LMARK(2,IMRK))
        DO 200 J=1,3
200        LMARK(J,77) = (LMARK(J,42) + LMARK(J,43))/2.
        LMKNM(1,77) = 10H(42 + 43)/
        LMKNM(2,77) = 10H2

        CALL WTITLE (1,.FALSE.,1)
        WRITE (6,66)
        DO 300 I=1,38
300        WRITE (6,SEVEN) I,(LMKNM(J,I),J=1,2),(LMARK(J,I),J=1,3)
        WRITE (6,55)
        CALL WTITLE (1,.TRUE.,1)
        WRITE (6,66)
        DO 400 I=39,77
400        WRITE (6,SEVEN) I,(LMKNM(J,I),J=1,2),(LMARK(J,I),J=1,3)
        WRITE (6,55)

        RETURN
55      FORMAT (////20X,*IF X=Y=Z=0.0 THEN POINT WAS NOT OBTAINED*)
66      FORMAT (30X,*LANDMARKS (UNITS: C.G.S.)*/30X,*WITH RESPECT TO *,
       &        *GLOBAL AXES*//15X,*#*,27X,*X*,10X,*Y*,10X,*Z*/)
77      FORMAT (46X,I3)
88      FORMAT (5X,A10,I15)
99      FORMAT (10X,2A10,3F10.2)
        END
```

```
*   SUBROUTINE WTB134 IS CALLED TO WRITE OUT TABLES 13 AND 14.
C
C
      SUBROUTINE WTB134
      COMMON /EIGEN/ TEN(25,3,3)
      COMMON /AAXES/ DUM(504),DCOSAP(9,25)
      COMMON /NAMES/ ISUB,SEGNM(25)
      REAL NAME

      CALL WTITLE (13,.FALSE.,3)
      WRITE (6,99)
      DO 100 ISEG=1,13
100      CALL TBLCOS(DCOSAP(1,ISEG),ISEG)
      CALL WTITLE (13,.TRUE.,3)
      WRITE (6,99)
      DO 200 ISEG=14,25
200      CALL TBLCOS (DCOSAP(1,ISEG),ISEG)

      CALL WTITLE (14,.FALSE.,1)
      WRITE (6,88)
      DO 300 ISEG=1,13
         NAME = SEGNM(ISEG)
         WRITE (6,77)
         DO 300 J=1,3
            WRITE (6,77) NAME,(TEN(ISEG,J,I),I=1,3)
300         NAME = 10H
      CALL WTITLE (14,.TRUE.,1)
      WRITE (6,88)
      DO 400 ISEG=14,24
         NAME = SEGNM(ISEG)
         WRITE (6,77)
         DO 400 J=1,3
            WRITE (6,77) NAME,(TEN(ISEG,J,I),I=1,3)
400         NAME = 10H
      WRITE (6,66)
      NAME = SEGNM(25)
      WRITE (6,77)
      DO 500 J=1,3
         WRITE (6,77) NAME,(TEN(25,J,I),I=1,3)
500      NAME = 10H

      RETURN
66    FORMAT (//14X,*TOTAL BODY*)
77    FORMAT (14X,A8,3(F12.0,5X))
88    FORMAT (10X,*SEGMENT INERTIAL TENSOR AT SEGMENT CENTER OF GRAVITY*
     &        /30X,*WITH RESPECT TO GLOBAL AXES*//14X,*SEGMENTS*)
99    FORMAT (10X,*DIRECTION COSINES (ANGLES) OF SEGMENT ANATOMICAL *,
     &         *AXES*/20X,*WITH RESPECT TO SEGMENT PA AXES*/
     &         31X,*(RA) = [DAG] [DGP] (RP)*/14X,*SEGMENTS*/)
      END
```

```
*     SUBROUTINE ALIGN COMPUTES THE DIRECTION COSINES OF THE SEGMENT PRIN-
C        CIPAL AXES SYSTEMS, BY PERMUTING ROWS OF THE MATRIX CONTAINING THE
C        DIRECTIONS OF THE PRINCIPAL MOMENTS.  THESE ROWS ARE PERMUTTED SO
C        THAT THE RESULTING PRINCIPAL AXES SYSTEM HAS THE BEST POSSIBLE
C        ALIGNMENT WITH THE CORRESPONDING SEGMENT ANATOMICAL AXES SYSTEM.
C        THE CHOSEN PERMUTATION IS ALSO APPLIED TO THE PRINCIPAL MOMENT
C        VECTOR.
C
C     PARAMETERS
C
C     DAG--DIRECTION COSINES OF THE ANATOMICAL WITH RESPECT TO GLOBAL AXES
C        AXES.
C     DPG--INITIALLY THE THREE VECTORS SPECIFYING THE DIRECTIONS OF THE
C        PRINCIPAL MOMENTS.  AT COMPLETION OF THE ROUTINE THIS IS THE
C        DIRECTION COSINE MATRIX OF THE PRINCIPAL W.R.T GLOBAL AXES.
C     DAP--DIRECTION COSINES OF THE ANATOMICAL W.R.T. PRINCIPAL AXES.
C     PMOM--THE VECTOR OF PRINCIPAL MOMENTS.
C
C
        SUBROUTINE ALIGN (DAG,DPG,DAP,PMOM)
        REAL DPG(3,3),DAG(3,3),DPA(3,3),PMOM(3),TMOM(3),TCOS(3,3),
     +     TCOS2(3,3),DAP(3,3),DGA(3,3)
        INTEGER COL(3),IN,R,R2,C,C2

        CALL TRNSP (DAG,DGA)
        CALL MATMUL (DPG,DGA,DPA,3)

C       FIND LARGEST COSINE IN EACH VECTOR
        DO 380 J=1,3
        COL(J)=1
        DO 380 K=2,3
        IF (ABS(DPA(     J,COL(J))).GE.ABS(DPA(     J,K))) GOTO 380
        COL(J)=K
380     CONTINUE
        IF (ISIGN(COL(1),INT(DPA(     1,1))).EQ.1.AND.ISIGN(COL(2),INT(
     +     DPA(     2,2))).EQ.2.AND.ISIGN(COL(3),INT(DPA(     3,3))).EQ.3)
     +     GOTO 360
C       DPA IS NOT PROPERLY ALIGNED AND MUST BE ROTATED
        IF (COL(1).NE.COL(2).AND.COL(2).NE.COL(3).AND.COL(3).NE.COL(1))
     +     GOTO 370
C       PROBLEM SYSTEM ENCOUNTERED.  TWO VECTORS APPEAR TO BELONG IN THE
C       SAME ROW OF THE COSINE MATRIX BECAUSE OF ITS ALIGNMENT.  THE
C       FOLLOWING SECTION FINDS THE BEST POSITIONS FOR THE VECTORS.
        IN=1
        IF (ABS(DPA(     2,COL(2))).GT.ABS(DPA(     1,COL(1)))) IN=2
        IF (ABS(DPA(     3,COL(3))).GT.ABS(DPA(     IN,COL(IN)))) IN=3
        R=IN
        C=COL(IN)
        DO 90 I=1,3
        IF (I.EQ.IN) GOTO 90
        DO 100 J=1,3
        IF (J.EQ.COL(IN)) GOTO 100
        IF (ABS(DPA(R,C)).LE.ABS(DPA(I,J))) GOTO 100
        R=I
        C=J
100     CONTINUE
90      CONTINUE
        R2=C2=0
110     R2=R2+1
        IF (R2.EQ.IN.OR.R2.EQ.R) GOTO 110
120     C2=C2+1
        IF (C2.EQ.COL(IN).OR.C2.EQ.C) GOTO 120
```

```
      COL(R)=C2
      COL(R2)=C
      IF (ISIGN(COL(1),INT(DPA(     1,1))).EQ.1.AND.ISIGN(COL(2),INT(
     +   DPA(     2,2))).EQ.2.AND.ISIGN(COL(3),INT(DPA(     3,3))).EQ.3)
     +   GOTO 360
C     TRANSFER VECTORS TO PROPER POSITION IN MATRIX  (ROTATE MATRIX)
370   DO 415 J=1,3
      TMOM(J)=PMOM(   J)
      DO 415 K=1,3
      TCOS2(J,K)=DPG(J,K)
415   TCOS(J,K)=DPA(    J,K)
      DO 430 J=1,3
      PMOM(   COL(J))=TMOM(J)
      DO 430 K=1,3
      DPG(COL(J),K)=TCOS2(J,K)*SIGN(1.,TCOS (J,COL(J)))
430   DPA(    COL(J),K)=TCOS(J,K)*SIGN(1.,TCOS(    J,COL(J)))
360   CALL TRNSP (DPA,DAP)
      RETURN
      END
```

```
*    SUBROUTINE COMBI CONTROLS THE COMBINATION OF PRINCIPAL MOMENTS AND
C      THEIR DIRECTIONS FOR COMBINED SEGMENTS FROM THEIR ELEMENTAL SEG-
C      MENTS.
C
C
       SUBROUTINE COMBMI
       COMMON /EIGEN/ TEN(25,3,3)
       DO 10 NOSE = 20,25
          DO 10 I=1,3
             DO 10 J=1,3
10              TEN(NOSE,I,J) = 0.

       DO 100 NOSE=7,8
100       CALL TBOD(NOSE,20)
       DO 200 NOSE=10,11
200       CALL TBOD(NOSE,21)
       DO 300 NOSE=12,13
300       CALL TBOD(NOSE,22)
       DO 400 NOSE=16,17
400       CALL TBOD(NOSE,23)
       DO 500 NOSE=3,5
500       CALL TBOD(NOSE,24)
       DO 600 NOSE=1,19
600       CALL TBOD(NOSE,25)
       DO 700 NOSE=20,25
700       CALL EIGEN (NOSE)
       RETURN
       END


C    SUBROUTINE TBOD IS CALLED BY SUBROUTINE COMBI TO ADD THE INERTIAL
C      TENSOR FOR SEGMENT NOSEI TO THE INERTIAL TENSOR OF SEGMENT NOSEO
C      BY USE OF THE PARALLEL AXIS THEOREM.
C
C
       SUBROUTINE TBOD (NOSEI,NOSEO)
       COMMON /1/ XYZCG(25,3),VOL(25)
       COMMON /EIGEN/ TEN(25,3,3),EIGVEC(25,3,3),EIGR(25,3)
       DIMENSION ABC0(3)

       DO 100 I=1,3
100       ABC0(I) = XYZCG(NOSEI,I) - XYZCG(NOSEO,I)
       DO 300 I=1,3
          DO 300 J=1,3
             IF (I.EQ.J) GOTO 200
                RH = -ABC0(I)*ABC0(J)
                GOTO 300
200          IF (I - 2) 225,250,275
225             RH = ABC0(2)**2 + ABC0(3)**2
                GOTO 300
250             RH = ABC0(1)**2 + ABC0(3)**2
                GOTO 300
275             RH = ABC0(1)**2 + ABC0(2)**2
300          TEN(NOSEO,I,J) = TEN(NOSEO,I,J) + TEN(NOSEI,I,J)
     &                       + VOL(NOSEI)*RH
       RETURN
       END
```

```
*   SUBROUTINE EIGEN WAS WRITTEN BY MEMBERS OF THE AFAMRL/BBM.  IT IS
C     INCLUDED HERE SINCE IT IS CALLED BY SUBROUTINE COMBI.
C
C
      SUBROUTINE  EIGEN(NOSE)
      COMMON/EIGEN/ TEN(25,3,3),EIGVEC(25,3,3),EIGR(25,3)
      DIMENSION  A(3,3),Z(3,3),D(3),DD(3),WR(3),WI(3)

*   IN THE FOLLOWING SUBROUTINE, EIGENVALUES AND EIGENVECTORS OF A REAL
*     MATRIX ARE COMPUTED.  THIS IS ACCOMPLISHED BY FIRST CALLING EBALAF
*     TO PRECONDITION THE FULL MATRIX.  THE RESULTANT MATRIX IS THEN
*     REDUCED TO UPPER HESSENBERG FORM BY CALLING EHESSF.  EHBCKF IS
*     THEN CALLED WITH THE IDENTITY MATRIX AS INPUT TO OBTAIN THE
*     TRANSFORMATION MATRIX PRODUCED IN EHESSF WHICH REDUCED THE GENERAL
*     MATRIX TO HESSENBERG FORM.  THIS TRANSFORMATION MATRIX AND THE
*     HESSENBERG MATRIX ARE THEN INPUT TO EQRH3F TO OBTAIN EIGENVALUES
*     AND EIGENVECTORS OF THE HESSENBERG MATRIX.  A CALL TO EBBCKF
*     BACKTRANSFORMS THE EIGENVECTORS OF THE BALANCED MATRIX TO FORM THE
*     EIGENVECTORS OF THE ORIGINAL MATRIX.

      DO 10  I=1,3
      DO 5  J=1,3
5     A(I,J)= TEN(NOSE,I,J)
10    CONTINUE
      N= 3
      MM= 3
      IA= 3
      IZ= 3
*     BALANCE MATRIX A PRIOR TO EIGENVALUE COMPUTATIONS
      CALL  EBALAF(A,N,IA,D,K,L)
*     REDUCE BALANCED MATRIX A TO HESSENBERG FORM
      CALL  EHESSF(A,K,L,N,IA,DD)
*     SET Z TO THE IDENTITY MATRIX
      DO 20  I=1,N
      DO 15  J=1,N
      Z(I,J)= 0.0
15    CONTINUE
      Z(I,I)= 1.0
20    CONTINUE
*     BACKTRANSFORMATION OF UPPER HESSENGERG MATRIX TO ITS ORIGINAL FORM
      CALL  EHBCKF(Z,A,DD,N,MM,IA,K,L)
*     COMPUTE ALL EIGENVALUES OF A HESSENBERG MATRIX.  THE VECTORS
*     WR AND WI OF LENGTH N CONTAIN THE REAL AND IMAGINARY PARTS OF THE
*     EIGENVALUES, RESPECTIVELY.  ON OUTPUT THE N BY N MATRIX Z CONTAINS
*     THE REAL PARTS OF THE EIGENVECTORS.
      CALL  EQRH3F(A,N,IA,K,L,WR,WI,Z,IZ,IER)
*     BACKTRANSFORMATION OF THE EIGENVECTORS OF THE BALANCED MATRIX TO
*     THOSE OF THE ORIGINAL INPUT MATRIX.
      CALL  EBBCKF(D,Z,K,L,MM,N,IZ)
      DO 30  I=1,3
      DO 25  J=1,3
25    EIGVEC(NOSE,I,J)= Z(J,I)
30    CONTINUE
      DO 70  I=1,3
70    EIGR(NOSE,I)= WR(I)
      RETURN
      END
```

```
*   SUBROUTINE WTBL34 IS CALLED TO WRITE OUT TABLES 3 AND 4.
C
C
      SUBROUTINE WTBL34
      COMMON /EIGEN/ TEN(225),EIGVEC(25,9),EIGR(25,3)
      COMMON /NAMES/ ISUB,SEGNM(25)
      REAL DCOS(9)

      CALL WTITLE (3,.FALSE.,2)
      WRITE (6,99)
      DO 100 ISEG=1,24
         IF ((ISEG-1)/3*3.EQ.ISEG-1) WRITE (6,88)
100      WRITE (6,88) SEGNM(ISEG),(EIGR(ISEG,J),J=1,3)
      WRITE (6,77)
      WRITE (6,88) SEGNM(25),(EIGR(25,J),J=1,3)
      WRITE (6,55)

      CALL WTITLE (4,.FALSE.,1)
      WRITE (6,66)
      DO 200 ISEG=1,13
         DO 190 J=1,9
190         DCOS(J) = EIGVEC(ISEG,J)
200      CALL TBLCOS (DCOS,ISEG)
      CALL WTITLE (4,.TRUE.,1)
      WRITE (6,66)
      DO 300 ISEG=14,25
         DO 290 J=1,9
290         DCOS(J) = EIGVEC(ISEG,J)
300      CALL TBLCOS (DCOS,ISEG)

      RETURN
55    FORMAT (//////14X,"* ASSIGNED ACCORDING TO SEGMENT ANATO. AXES")
66    FORMAT (18X,*DIRECTION COSINES (ANGLES) OF SEGMENT PRINCIPAL AXES*
     &        /30X,*WITH RESPECT TO GLOBAL AXES*/34X,*(RP) : [DPG] (RG)*
     &        /14X,*SEGMENTS*/)
77    FORMAT (//14X,*TOTAL BODY*/)
88    FORMAT (14X,A8,3(F16.0,1X))
99    FORMAT (16X,*SEGMENT PRINCIPAL MOMENTS OF INERTIA (UNITS: C.G.S.)*
     &        /31X,*(PM) : [DPG] (IG) [DGP]*///15X,*NAME*,14X,5HIPX *,
     &        10X,5HIPY *,12X,5HIPZ *//14X,*SEGMENTS*)
      END


C   SUBROUTINE FTOM IS USED TO CONVERT X,Y COORDINATES TO THE ADJUSTED
C     GLOBAL AXES SYSTEM.
C
C
      SUBROUTINE FTOM (XF,YF)
      COMMON /TRANS/ XA,YA,COSR,SINR

      X0 = XF - XA
      Y0 = YF - YA
      XF = COSR*X0 + SINR*Y0
      YF =-SINR*X0 + COSR*Y0
      RETURN
      END
```

APPENDIX I

SAMPLE OF RESULTS CALCULATED BY PROGRAM IMPED

TABLE # 1 SUBJECT 11 GLOBAL AXES

LANDMARKS (UNITS: C.G.S.)
WITH RESPECT TO GLOBAL AXES

#		X	Y	Z
1	NUCHALE	-16.78	.22	156.65
2	CERVICALE	-15.21	.27	147.42
3	LEFT ACROMIALE	-14.52	18.82	139.72
4	RIGHT ACROMIALE	-12.77	-18.43	139.49
5	LEFT POS SCYE	-19.34	15.38	128.63
6	RIGHT POS SCYE	-17.72	-15.58	128.41
7	10TH RIBMIDSPINE	-16.58	.45	108.13
8	POS SUP ILIAC MS	-18.37	.01	101.02
9	L MED HUM EPICON	-8.38	19.25	108.05
10	R MED HUM EPICON	-6.40	-18.58	106.82
11	L LAT HUM EPICON	-14.39	23.83	109.89
12	R LAT HUM EPICON	-12.33	-23.65	109.16
13	LEFT OLECRANON	-13.08	19.68	108.79
14	RIGHT OLECRANON	-11.43	-18.86	107.97
15	LEFT RADIALE	-13.78	23.83	108.86
16	RIGHT RADIALE	-12.84	-23.67	107.17
17	L GLUTEAL FOLD	-19.79	7.58	77.81
18	R GLUTEAL FOLD	-19.95	-8.87	77.71
19	L ULNAR STYLOID	-11.32	31.37	85.27
20	R ULNAR STYLOID	-8.79	-31.86	84.37
21	L RADIAL STYLOID	-11.65	37.83	86.53
22	R RADIAL STYLOID	-8.66	-36.68	86.14
23	L METACARPALE II	-11.82	41.17	79.12
24	R METACARPALE II	-7.47	-41.83	79.19
25	L METACARPALEIII	-12.81	38.81	77.35
26	R METACARPALEIII	-7.86	-38.24	77.86
27	L METACARPALE V	-9.24	33.26	77.97
28	R METACARPALE V	-5.73	-33.48	77.21
29	LEFT DACTYLION	-18.29	48.59	67.99
30	RIGHT DACTYLION	-5.45	-41.44	67.85
31	L POS CALCANEUS	-20.81	12.62	1.22
32	R POS CALCANEUS	-20.74	-12.57	1.21
33	HEAD CIRC	.42	.59	165.68
34	SELLION	.98	.77	161.99
35	L INFRAORBITALE	-.78	4.88	168.31
36	R INFRAORBITALE	-.63	.17	168.12
37	LEFT TRAGION	-8.14	7.57	158.84
38	RIGHT TRAGION	-7.77	-6.75	158.88

IF X=Y=Z=0.0 THEN POINT WAS NOT OBTAINED

TABLE # 1 (CONTINUED) SUBJECT 11 GLOBAL AXES

LANDMARKS (UNITS: C.G.S.)
WITH RESPECT TO GLOBAL AXES

#		X	Y	Z
39	LEFT GONION	-7.03	6.00	153.10
40	RIGHT GONION	-6.03	-5.19	153.16
41	MID THYROID CART	-4.51	.62	146.85
42	LEFT CLAVICALE	-5.08	3.34	142.83
43	RIGHT CLAVICALE	-4.81	-2.13	142.76
44	SUPRASTERNALE	-4.12	.66	141.59
45	LEFT ANT SCYE	-7.41	16.13	128.26
46	RIGHT ANT SCYE	-5.90	-15.12	128.42
47	LEFT BUSTPOINT	5.62	10.57	125.04
48	RIGHT BUSTPOINT	6.64	-8.51	124.75
49	LEFT 10TH RIB	-9.07	13.10	109.11
50	RIGHT 10TH RIB	-9.05	-12.72	108.98
51	L ILIOCRISTALE	-8.03	15.31	104.91
52	R ILIOCRISTALE	-8.66	-14.26	106.39
53	LEFT ASIS	.00	12.67	94.72
54	RIGHT ASIS	.00	-12.67	95.27
55	SYMPHYSION	1.00	.37	86.95
56	L TROCHANTERION	-8.14	17.85	88.81
57	R TROCHANTERION	-9.16	-18.30	89.87
58	L LAT FEM CONDYL	-13.80	14.51	48.81
59	R LAT FEM CONDYL	-11.98	-15.32	48.67
60	L MED FEM CONDYL	-14.47	3.23	47.30
61	R MED FEM CONDYL	-12.10	-3.96	47.29
62	LEFT TIBIALE	-13.23	5.16	44.33
63	RIGHT TIBIALE	-11.56	-5.57	44.28
64	LEFT FIBULARE	-16.13	15.14	44.31
65	RIGHT FIBULARE	-13.09	-15.69	44.53
66	L LAT MALLEOLUS	-16.16	15.72	7.24
67	R LAT MALLEOLUS	-16.74	-15.20	7.08
68	LEFT SPHYRION	-12.70	10.81	6.71
69	RIGHT SPHYRION	-13.23	-9.00	6.31
70	L METATARSAL I	-2.34	9.45	2.33
71	R METATARSAL I	-1.92	-9.11	2.27
72	L METATARSAL V	-4.09	18.57	.98
73	R METATARSAL V	-4.69	-18.86	.68
74	LEFT TOE II	3.71	13.70	.12
75	RIGHT TOE II	4.04	-13.92	.40
76	CROTCH SENSOR	-5.33	.07	79.20
77	(42 + 43)/2	-4.95	.60	142.80

IF X=Y=Z=0.0 THEN POINT WAS NOT OBTAINED

TABLE # 2 SUBJECT 11 GLOBAL AXES

VOLUME AND CENTER OF GRAVITY (UNITS: C.G.S.)
WITH RESPECT TO GLOBAL AXES

NAME	VOLUME	% VOL.	X C.G.	Y C.G.	Z C.G.
SEGMENTS					
HEAD	4150.8	5.53	-8.59	.19	162.32
NECK	851.2	1.13	-9.17	.33	150.25
THORAX	20704.7	27.59	-9.49	.30	126.31
ABDOMEN	809.3	1.08	-7.61	.17	107.41
PELVIS	11309.7	15.07	-8.96	-.08	97.20
RU ARM	1827.1	2.43	-10.66	-19.16	122.27
RF ARM	1044.9	1.39	-8.46	-26.94	98.52
R HAND	426.0	.57	-6.43	-36.91	80.51
LU ARM	1755.6	2.34	-12.57	19.60	123.34
LF ARM	1108.0	1.48	-11.03	27.47	99.54
L HAND	414.4	.55	-10.11	37.03	80.44
R FLAP	4456.8	5.94	-10.46	-9.79	84.71
R THI-F	6529.5	8.70	-10.23	-9.62	66.22
R CALF	3809.8	5.08	-15.47	-11.54	31.83
R FOOT	792.1	1.06	-9.85	-12.80	2.64
L FLAP	4008.1	5.34	-10.90	9.17	84.52
L THI-F	6463.9	8.61	-11.24	9.12	66.05
L CALF	3754.4	5.00	-17.00	11.21	31.78
L FOOT	819.2	1.09	-9.85	13.20	2.64
R FARM+H	1470.9	1.96	-7.87	-29.83	93.31
L FARM+H	1522.4	2.03	-10.70	30.07	94.34
R THIGH	10986.3	14.64	-10.32	-9.69	73.72
L THIGH	10472.0	13.96	-11.11	9.14	73.12
TORSO	32823.6	43.74	-9.26	.16	115.81
TOTAL BODY					
TOT BODY	75035.3	100.00	-10.46	-.06	95.21

TABLE # 3 SUBJECT 11 PRINCIPAL AXES

SEGMENT PRINCIPAL MOMENTS OF INERTIA (UNITS: C.G.S.)
(PM) = [DPG] (IG) [DGP]

NAME	IPX *	IPY *	IPZ *
SEGMENTS			
HEAD	194675.	210758.	141101.
NECK	12211.	15539.	17158.
THORAX	3324355.	2720775.	2139169.
ABDOMEN	41754.	23441.	64332.
PELVIS	1066000.	744702.	1277700.
RU ARM	123607.	120131.	22251.
RF ARM	48546.	46825.	8488.
R HAND	11754.	9950.	2071.
LU ARM	109600.	114034.	22074.
LF ARM	56630.	54392.	9245.
L HAND	10029.	9168.	2688.
R FLAP	172222.	220170.	294630.
R THI-F	592142.	610984.	254951.
R CALF	489676.	493072.	66630.
R FOOT	6470.	30031.	30970.
L FLAP	145401.	195299.	251655.
L THI-F	596152.	606791.	249070.
L CALF	480414.	484067.	65156.
L FOOT	6850.	31630.	32535.
R FARM+H	189613.	186405.	11470.
L FARM+H	205136.	201561.	12069.
R THIGH	1662969.	1740300.	552000.
L THIGH	1577395.	1649121.	506953.
TORSO	10663103.	9740355.	3500520.
TOTAL BODY			
TOT BODY	115359007.	107614476.	12510667.

* ASSIGNED ACCORDING TO SEGMENT ANATO. AXES

TABLE # 4 SUBJECT 11 GLOBAL AXES

DIRECTION COSINES (ANGLES) OF SEGMENT PRINCIPAL AXES
WITH RESPECT TO GLOBAL AXES
(RP) = [DPG] (RG)

SEGMENTS			
HEAD	.76096(40.5)	.12019(83.1)	.63756(50.4)
	-.14456(98.3)	.98940(8.4)	-.01398(90.8)
	-.63248(129.2)	-.08153(94.7)	.77027(39.6)
NECK	.83501(33.4)	.11315(83.5)	-.53847(122.6)
	-.10289(95.9)	.99349(6.5)	.05046(87.1)
	.54068(57.3)	.01284(89.3)	.84113(32.7)
THORAX	.97543(12.7)	.02130(88.8)	.21926(77.3)
	-.01333(90.8)	.99920(2.3)	-.03777(92.2)
	-.21988(102.7)	.03392(88.1)	.97494(12.9)
ABDOMEN	1.00000(.1)	-.00106(90.1)	-.00053(90.0)
	.00106(89.9)	1.00000(.1)	.00044(90.0)
	.00053(90.0)	-.00044(90.0)	1.00000(.0)
PELVIS	.94940(18.3)	-.03696(92.1)	.31190(71.8)
	.04096(87.7)	.99914(2.4)	-.00629(90.4)
	-.31140(108.1)	.01874(88.9)	.95010(18.2)
RU ARM	.98808(8.9)	-.06819(93.9)	.13800(82.1)
	.08193(85.3)	.99196(7.3)	-.09645(95.5)
	-.13032(97.5)	.10660(83.9)	.98572(9.7)
RF ARM	.93570(20.6)	-.29050(106.9)	.19981(78.5)
	.34984(69.5)	.83555(33.3)	-.42364(115.1)
	-.04380(92.5)	.46633(62.2)	.88352(27.9)
R HAND	.99428(6.1)	.05815(86.7)	.08957(84.9)
	-.01254(90.7)	.89650(26.3)	-.44287(116.3)
	-.10686(96.1)	.43921(63.9)	.89218(26.9)
LU ARM	.95370(17.5)	.25706(75.1)	.15564(81.0)
	-.27312(105.9)	.95755(16.8)	.09224(84.7)
	-.12532(97.2)	-.13049(97.5)	.98350(10.4)
LF ARM	.92231(22.7)	.35040(69.5)	.16297(80.6)
	-.38637(112.7)	.82775(34.1)	.40688(66.0)
	.00760(89.6)	-.43824(116.0)	.89883(26.0)
L HAND	.99951(1.8)	.01320(89.2)	.02836(88.4)
	-.02287(91.3)	.92823(21.8)	.37130(68.2)
	-.02139(91.2)	-.37177(111.8)	.92800(21.9)
R FLAP	.98955(8.3)	-.14243(98.2)	.02234(88.7)
	.14368(81.7)	.96145(16.0)	-.23445(103.6)
	.01192(89.3)	.23521(76.4)	.97187(13.6)
R THI-F	.98783(8.9)	-.01855(91.1)	-.15446(98.9)
	.02596(88.5)	.99860(3.0)	.04614(87.4)
	.15330(81.2)	-.04959(92.8)	.98692(9.3)

TABLE # 4 (CONTINUED) SUBJECT 11 GLOBAL AXES

DIRECTION COSINES (ANGLES) OF SEGMENT PRINCIPAL AXES
WITH RESPECT TO GLOBAL AXES
(RP) = [DPG] (RG)

SEGMENTS			
R CALF	.96478(15.3)	.24905(75.6)	-.08473(94.9)
	-.25376(104.7)	.96596(15.0)	-.05020(92.9)
	.06935(86.0)	.06993(86.0)	.99514(5.7)
R FOOT	.98865(8.6)	-.05376(93.1)	-.14030(98.1)
	.11497(83.4)	.87187(29.3)	.47606(61.6)
	.09673(84.4)	-.48678(119.1)	.86815(29.8)
L FLAP	.96860(14.4)	.24426(75.9)	.04628(87.3)
	-.24835(104.4)	.94212(19.6)	.22523(77.0)
	.01141(89.3)	-.22965(103.3)	.97321(13.3)
L THI-F	.95367(17.5)	.20635(78.1)	-.21892(102.6)
	-.20964(102.1)	.97774(12.1)	.00830(89.5)
	.21578(77.5)	.03790(87.8)	.97571(12.7)
L CALF	.99750(4.1)	-.06481(93.7)	-.02814(91.6)
	.06725(86.1)	.99306(6.8)	.09649(84.5)
	.02169(88.8)	-.09814(95.6)	.99494(5.8)
L FOOT	.99033(8.0)	.04855(87.2)	-.12995(97.5)
	-.10093(95.8)	.89481(26.5)	-.43489(115.8)
	.09516(84.5)	.44381(63.7)	.89106(27.0)
R FARM+H	.98252(10.7)	-.10458(96.0)	.15398(81.1)
	.16492(80.5)	.87264(29.2)	-.45968(117.4)
	-.08629(95.0)	.47704(61.5)	.87464(29.0)
L FARM+H	.97169(13.7)	.19741(78.6)	.12980(82.5)
	-.23437(103.6)	.87475(29.0)	.42413(64.9)
	-.02982(91.7)	-.44255(116.3)	.89625(26.3)
R THIGH	.99288(6.8)	-.11218(96.4)	-.04007(92.3)
	.11344(83.5)	.99308(6.7)	.03042(88.3)
	.03638(87.9)	-.03475(92.0)	.99873(2.9)
L THIGH	.97425(13.0)	.20747(78.0)	-.08824(95.1)
	-.20894(102.1)	.97790(12.1)	-.00774(90.4)
	.08468(85.1)	.02597(88.5)	.99607(5.1)
TORSO	.99903(2.5)	-.00010(90.0)	.04400(87.5)
	.00075(90.0)	.99989(.8)	-.01460(90.8)
	-.04399(92.5)	.01462(89.2)	.99892(2.7)

TOTAL BODY

TOT BODY	.99838(3.3)	.04282(87.5)	-.03754(92.2)
	-.04299(92.5)	.99907(2.5)	-.00387(90.2)
	.03734(87.9)	.00547(89.7)	.99929(2.2)

TABLE # 5 SUBJECT 11 GLOBAL AXES

ORIGIN OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO GLOBAL AXES

SEG	X	Y	Z
HEAD	-7.96	.55	150.82
NECK	-15.21	.27	147.42
THORAX	-16.58	.45	180.13
ABDOMEN	-9.86	.45	109.05
PELVIS	.00	-.12	95.00
RU ARM	-12.77	-18.43	139.49
RF ARM	-12.04	-23.67	107.17
R HAND	-6.81	-30.12	78.44
LU ARM	-14.52	18.82	139.72
LF ARM	-13.78	23.83	108.06
L HAND	-10.35	30.19	78.69
R FLAP	-9.16	-10.30	89.87
R THI-F	-9.16	-10.30	89.87
R CALF	-11.56	-5.57	44.28
R FOOT	-2.20	-13.73	1.40
L FLAP	-8.14	17.05	88.81
L THI-F	-8.14	17.05	88.81
L CALF	-13.23	5.16	44.33
L FOOT	-2.55	13.62	1.71
R FARM+H	-12.04	-23.67	107.17
L FARM+H	-13.78	23.83	108.06
R THIGH	-9.16	-10.30	89.87
L THIGH	-8.14	17.05	88.81
TORSO	.00	-.12	95.00

TOTAL BODY

TOT BODY	.00	-.12	95.00

TABLE # 6 SUBJECT 11 GLOBAL AXES

DIRECTION COSINES (ANGLES) OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO GLOBAL AXES
(RA) = [DAG] (RG)

SEGMENTS			
HEAD	.98424(10.2)	.02465(88.6)	.17512(79.9)
	-.02553(91.5)	.99967(1.5)	.00279(89.8)
	-.17500(100.1)	-.00722(90.4)	.98454(10.1)
NECK	.91117(24.3)	.03222(88.2)	-.41077(114.3)
	-.03263(91.9)	.99945(1.9)	.00600(89.7)
	.41074(65.7)	.00793(89.5)	.91172(24.3)
THORAX	.99880(2.8)	.03296(88.1)	-.03487(92.0)
	-.03279(91.9)	.99945(1.9)	.00572(89.7)
	.03504(88.0)	-.00457(90.3)	.99938(2.0)
ABDOMEN	.99266(6.9)	.00005(90.0)	.12096(83.1)
	-.00067(90.0)	.99999(.3)	.00504(89.7)
	-.12096(96.9)	-.00500(90.3)	.99264(7.0)
PELVIS	.97575(12.6)	.00475(89.7)	.21805(77.4)
	.00000(90.0)	.99976(1.2)	-.02169(91.2)
	-.21890(102.6)	.02117(88.8)	.97552(12.7)
RU ARM	.67432(47.6)	-.72601(136.6)	.13495(82.2)
	.73830(42.4)	.66639(48.2)	-.10409(96.0)
	-.01436(90.8)	.16983(80.2)	.98537(9.8)
RF ARM	.99072(7.8)	.07124(85.9)	.11575(83.4)
	-.02769(91.6)	.93955(20.0)	-.34129(110.0)
	-.13307(97.6)	.33492(70.4)	.93280(21.1)
R HAND	.96819(14.5)	-.17441(100.0)	.17943(79.7)
	.21572(77.5)	.94514(19.1)	-.24530(104.2)
	-.12680(97.3)	.27620(74.0)	.95270(17.7)
LU ARM	.62612(51.2)	.76849(39.8)	.13192(82.4)
	-.77972(141.2)	.61799(51.8)	.10066(84.2)
	-.00416(90.2)	-.16509(99.5)	.98614(9.6)
LF ARM	.99260(7.0)	.03139(88.2)	.11731(83.3)
	-.06632(93.8)	.94934(18.3)	.30716(72.1)
	-.10173(95.8)	-.31267(108.2)	.94440(19.2)
L HAND	.97581(12.6)	.21203(77.8)	.05321(86.9)
	-.21753(102.6)	.96590(15.0)	.14043(81.9)
	-.02162(91.2)	-.14861(98.5)	.98866(8.6)
R FLAP	.99766(3.9)	.00907(89.5)	-.06771(93.9)
	-.00402(90.2)	.99723(4.3)	.07430(85.7)
	.06820(86.1)	-.07306(94.2)	.99493(5.8)
R THI-F	.99766(3.9)	.00907(89.5)	-.06771(93.9)
	-.00402(90.2)	.99723(4.3)	.07430(85.7)
	.06820(86.1)	-.07306(94.2)	.99493(5.8)

TABLE # 6 (CONTINUED) SUBJECT 11 GLOBAL AXES

DIRECTION COSINES (ANGLES) OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO GLOBAL AXES
(RA) = [DAG] (RG)

SEGMENTS			
R CALF	.87898(29.4)	-.49127(119.4)	.00697(89.6)
	.48936(60.7)	.86616(30.0)	-.10148(95.8)
	.04382(87.5)	.09180(84.7)	.99481(5.8)
R FOOT	.99796(3.7)	-.06212(93.6)	.01445(89.2)
	.05888(86.6)	.98391(10.3)	.16878(80.3)
	-.02478(91.4)	-.16751(99.6)	.98556(9.7)
L FLAP	.98974(8.2)	-.04204(92.4)	-.13657(97.8)
	.03023(88.3)	.99571(5.3)	-.08742(95.0)
	.13966(82.0)	.08239(85.3)	.98677(9.3)
L THI-F	.98974(8.2)	-.04204(92.4)	-.13657(97.8)
	.03023(88.3)	.99571(5.3)	-.08742(95.0)
	.13966(82.0)	.08239(85.3)	.98677(9.3)
L CALF	.85596(31.1)	.51114(59.3)	.07792(85.5)
	-.51685(121.1)	.84996(31.8)	.10210(84.1)
	-.01404(90.8)	-.12766(97.3)	.99172(7.4)
L FOOT	.99815(3.5)	.05462(86.9)	.02673(88.5)
	-.05012(92.9)	.98787(8.9)	-.14699(98.5)
	-.03444(92.0)	.14538(81.6)	.98878(8.6)
R FARM+H	.99072(7.8)	.07124(85.9)	.11575(83.4)
	-.02769(91.6)	.93955(20.0)	-.34129(110.0)
	-.13307(97.6)	.33492(70.4)	.93280(21.1)
L FARM+H	.99260(7.0)	.03139(88.2)	.11731(83.3)
	-.06632(93.8)	.94934(18.3)	.30716(72.1)
	-.10173(95.8)	-.31267(108.2)	.94440(19.2)
R THIGH	.99766(3.9)	.00907(89.5)	-.06771(93.9)
	-.00402(90.2)	.99723(4.3)	.07430(85.7)
	.06820(86.1)	-.07386(94.2)	.99493(5.8)
L THIGH	.98974(8.2)	-.04204(92.4)	-.13657(97.8)
	.03023(88.3)	.99571(5.3)	-.08742(95.0)
	.13966(82.0)	.08239(85.3)	.98677(9.3)
TORSO	.97575(12.6)	.00475(89.7)	.21885(77.4)
	.00000(90.0)	.99976(1.2)	-.02169(91.2)
	-.21890(102.6)	.02117(88.8)	.97552(12.7)

TOTAL BODY

TOT BODY	.97575(12.6)	.00475(89.7)	.21885(77.4)
	.00000(90.0)	.99976(1.2)	-.02169(91.2)
	-.21890(102.6)	.02117(88.8)	.97552(12.7)

TABLE # 7 SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT HEAD	
37	LEFT TRAGION	-.98	7.28	-3.57
38	RIGHT TRAGION	-2.45	-6.94	-2.66
36	R INFRAORBITALE	4.66	-1.14	-6.73
37	LEFT TRAGION	-.98	7.28	-3.57
38	RIGHT TRAGION	-2.45	-6.94	-2.66
34	SELLION	7.15	-.81	-6.35
LANDMARKS				
1	NUCHALE	-9.84	1.29	.81
34	SELLION	7.15	-.81	-6.35
36	R INFRAORBITALE	4.66	-1.14	-6.73
37	LEFT TRAGION	-.98	7.28	-3.57
38	RIGHT TRAGION	-2.45	-6.94	-2.66
39	LEFT GONION	-3.99	5.65	-8.56
40	RIGHT GONION	-5.14	-5.45	-7.73
ANATOMICAL SYSTEM ORIGIN				
0		-1.70	.31	-3.12
AXES DEFINITION POINTS			SEGMENT NECK	
41	MID THYROID CART	5.75	-.36	-.34
2	CERVICALE	-3.53	.41	-5.65
44	SUPRASTERNALE	8.91	-.62	-4.55
77	(42 + 43)/2	7.57	-.54	-3.99
2	CERVICALE	-3.53	.41	-5.65
2	CERVICALE	-3.53	.41	-5.65
LANDMARKS				
1	NUCHALE	-9.82	.99	1.26
2	CERVICALE	-3.53	.41	-5.65
39	LEFT GONION	.89	5.56	3.62
40	RIGHT GONION	-.24	-5.58	3.64
41	MID THYROID CART	5.75	-.36	-.34
42	LEFT CLAVICALE	7.75	2.28	-4.00
43	RIGHT CLAVICALE	7.39	-3.27	-3.98
44	SUPRASTERNALE	8.91	-.62	-4.55
ANATOMICAL SYSTEM ORIGIN				
0		-3.53	.41	-5.65

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT THORAX	
44	SUPRASTERNALE	8.59	-.28	13.73
2	CERVICALE	-.95	-.75	21.84
7	10TH RIBMIDSPINE	-10.90	.93	-16.15
2	CERVICALE	-.95	-.75	21.84
7	10TH RIBMIDSPINE	-10.90	.93	-16.15
7	10TH RIBMIDSPINE	-10.90	.93	-16.15
LANDMARKS				
2	CERVICALE	-.95	-.75	21.84
3	LEFT ACROMIALE	-1.57	18.06	14.81
4	RIGHT ACROMIALE	-.71	-19.16	12.94
5	LEFT POS SCYE	-8.78	15.83	4.94
6	RIGHT POS SCYE	-7.98	-15.83	3.32
7	10TH RIBMIDSPINE	-10.90	.93	-16.15
42	LEFT CLAVICALE	7.98	2.36	15.25
43	RIGHT CLAVICALE	8.12	-3.11	14.93
44	SUPRASTERNALE	8.59	-.28	13.73
45	LEFT ANT SCYE	2.79	15.72	1.99
46	RIGHT ANT SCYE	3.63	-15.53	.75
49	LEFT 10TH RIB	-3.89	13.44	-16.42
50	RIGHT 10TH RIB	-3.65	-12.35	-17.43
ANATOMICAL SYSTEM ORIGIN				
0		-10.90	.93	-16.15
AXES DEFINITION POINTS			SEGMENT ABDOMEN	
49	LEFT 10TH RIB	-1.48	12.93	1.78
50	RIGHT 10TH RIB	-1.43	-12.80	1.58
7	10TH RIBMIDSPINE	-8.97	.27	.72
49	LEFT 10TH RIB	-1.48	12.93	1.78
50	RIGHT 10TH RIB	-1.43	-12.80	1.58
7	10TH RIBMIDSPINE	-8.97	.27	.72
LANDMARKS				
7	10TH RIBMIDSPINE	-8.97	.27	.72
8	POS SUP ILIAC MS	-10.75	-.17	-6.39
49	LEFT 10TH RIB	-1.48	12.93	1.78
50	RIGHT 10TH RIB	-1.43	-12.80	1.58
51	L ILIOCRISTALE	-1.24	15.14	-2.58
52	R ILIOCRISTALE	-1.83	-14.43	-1.81
ANATOMICAL SYSTEM ORIGIN				
0		-1.46	.28	1.64

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT PELVIS	
53	LEFT ASIS	7.26	13.13	-4.91
54	RIGHT ASIS	8.37	-12.20	-4.86
55	SYMPHYSION	7.00	.96	-13.08
53	LEFT ASIS	7.26	13.13	-4.91
54	RIGHT ASIS	8.37	-12.20	-4.86
8	POS SUP ILIAC MS	-7.74	-.32	6.56
LANDMARKS				
8	POS SUP ILIAC MS	-7.74	-.32	6.56
51	L ILIOCRISTALE	1.96	15.34	7.57
52	R ILIOCRISTALE	3.68	-14.21	8.37
53	LEFT ASIS	7.26	13.13	-4.91
54	RIGHT ASIS	8.37	-12.20	-4.86
55	SYMPHYSION	7.00	.96	-13.08
56	L TROCHANTERION	-2.50	18.00	-7.90
57	R TROCHANTERION	-1.80	-18.25	-7.25
ANATOMICAL SYSTEM ORIGIN				
0		7.82	.34	-4.89
AXES DEFINITION POINTS			SEGMENT RU ARM	
4	RIGHT ACROMIALE	.24	-1.10	17.33
10	R MED HUM EPICON	2.04	2.41	-15.72
12	R LAT HUM EPICON	-3.15	-3.33	-13.19
4	RIGHT ACROMIALE	.24	-1.10	17.33
12	R LAT HUM EPICON	-3.15	-3.33	-13.19
4	RIGHT ACROMIALE	.24	-1.10	17.33
LANDMARKS				
4	RIGHT ACROMIALE	.24	-1.10	17.33
6	RIGHT POS SCYE	-6.37	2.39	7.35
10	R MED HUM EPICON	2.04	2.41	-15.72
12	R LAT HUM EPICON	-3.15	-3.33	-13.19
14	RIGHT OLECRANON	-2.76	1.62	-13.96
16	RIGHT RADIALE	-3.15	-3.13	-15.19
46	RIGHT ANT SCYE	5.27	3.80	5.87
ANATOMICAL SYSTEM ORIGIN				
0		.24	-1.10	17.33

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT RF ARM	
20	R ULNAR STYLOID	-1.71	1.77	-14.78
22	R RADIAL STYLOID	.15	-2.98	-15.44
16	RIGHT RADIALE	-2.57	-2.19	9.32
20	R ULNAR STYLOID	-1.71	1.77	-14.78
16	RIGHT RADIALE	-2.57	-2.19	9.32
16	RIGHT RADIALE	-2.57	-2.19	9.32
LANDMARKS				
10	R MED HUM EPICON	1.16	4.19	11.14
12	R LAT HUM EPICON	-2.45	-3.12	11.10
14	RIGHT OLECRANON	-3.24	1.71	12.25
16	RIGHT RADIALE	-2.57	-2.19	9.32
20	R ULNAR STYLOID	-1.71	1.77	-14.78
22	R RADIAL STYLOID	.15	-2.98	-15.44
ANATOMICAL SYSTEM ORIGIN				
0		-2.57	-2.19	9.32
AXES DEFINITION POINTS			SEGMENT R HAND	
30	RIGHT DACTYLION	-.42	1.53	-13.39
24	R METACARPALE II	-1.39	-3.09	-2.88
28	R METACARPALE V	.60	4.60	-1.40
24	R METACARPALE II	-1.39	-3.09	-2.88
28	R METACARPALE V	.60	4.60	-1.40
26	R METACARPALEIII	-1.00	.36	-3.51
LANDMARKS				
20	R ULNAR STYLOID	-1.71	2.85	5.91
22	R RADIAL STYLOID	-1.69	-2.10	5.40
24	R METACARPALE II	-1.39	-3.09	-2.88
26	R METACARPALEIII	-1.00	.36	-3.51
28	R METACARPALE V	.60	4.60	-1.40
30	RIGHT DACTYLION	-.42	1.53	-13.39
ANATOMICAL SYSTEM ORIGIN				
0		-.63	-.16	-2.34

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT LU ARM	
3	LEFT ACROMIALE	.49	1.29	16.46
9	L MED HUM EPICON	1.53	-2.89	-15.51
11	L LAT HUM EPICON	-2.74	3.31	-13.55
3	LEFT ACROMIALE	.49	1.29	16.46
11	L LAT HUM EPICON	-2.74	3.31	-13.55
3	LEFT ACROMIALE	.49	1.29	16.46
LANDMARKS				
3	LEFT ACROMIALE	.49	1.29	16.46
5	LEFT POS SCYE	-6.74	-1.78	6.62
9	L MED HUM EPICON	1.53	-2.89	-15.51
11	L LAT HUM EPICON	-2.74	3.31	-13.55
13	LEFT OLECRANON	-2.65	-1.15	-14.26
15	LEFT RADIALE	-2.45	2.97	-15.42
45	LEFT ANT SCYE	4.79	-4.27	4.65
ANATOMICAL SYSTEM ORIGIN				
0		.49	1.29	16.46
AXES DEFINITION POINTS			SEGMENT LF ARM	
19	L ULNAR STYLOID	-1.23	-2.46	-14.54
21	L RADIAL STYLOID	.66	2.86	-15.89
15	LEFT RADIALE	-2.42	1.51	9.23
19	L ULNAR STYLOID	-1.23	-2.46	-14.54
15	LEFT RADIALE	-2.42	1.51	9.23
15	LEFT RADIALE	-2.42	1.51	9.23
LANDMARKS				
9	L MED HUM EPICON	.96	-4.36	11.27
11	L LAT HUM EPICON	-2.68	2.50	10.87
13	LEFT OLECRANON	-3.03	-1.92	11.71
15	LEFT RADIALE	-2.42	1.51	9.23
19	L ULNAR STYLOID	-1.23	-2.46	-14.54
21	L RADIAL STYLOID	.66	2.86	-15.89
ANATOMICAL SYSTEM ORIGIN				
0		-2.42	1.51	9.23

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L HAND	
29	LEFT DACTYLION	-.49	-1.31	-12.88
23	L METACARPALE II	-.98	3.37	-2.75
27	L METACARPALE V	.75	-4.44	-.91
23	L METACARPALE II	-.98	3.37	-2.75
27	L METACARPALE V	.75	-4.44	-.91
25	L METACARPALEIII	-1.97	-.19	-3.19
LANDMARKS				
19	L ULNAR STYLOID	-1.15	-3.43	6.61
21	L RADIAL STYLOID	-1.37	2.38	5.68
23	L METACARPALE II	-.98	3.37	-2.75
25	L METACARPALEIII	-1.97	-.19	-3.19
27	L METACARPALE V	.75	-4.44	-.91
29	LEFT DACTYLION	-.49	-1.31	-12.88
ANATOMICAL SYSTEM ORIGIN				
0		-.28	.43	-2.85
AXES DEFINITION POINTS			SEGMENT R FLAP	
57	R TROCHANTERION	2.63	-9.29	3.81
59	R LAT FEM CONDYL	-1.52	2.91	-36.34
61	R MED FEM CONDYL	-3.36	14.13	-35.82
59	R LAT FEM CONDYL	-1.52	2.91	-36.34
57	R TROCHANTERION	2.63	-9.29	3.81
57	R TROCHANTERION	2.63	-9.29	3.81
LANDMARKS				
18	R GLUTEAL FOLD	-9.68	1.16	-6.78
54	RIGHT ASIS	11.88	-3.75	9.71
55	SYMPHYSION	18.74	11.81	4.72
57	R TROCHANTERION	2.63	-9.29	3.81
ANATOMICAL SYSTEM ORIGIN				
0		2.63	-9.29	3.81

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT R THI-F	
57	R TROCHANTERION	-2.43	-7.63	23.94
59	R LAT FEM CONDYL	1.09	-6.55	-17.31
61	R MED FEM CONDYL	.89	4.72	-19.27
59	R LAT FEM CONDYL	1.09	-6.55	-17.31
57	R TROCHANTERION	-2.43	-7.63	23.94
57	R TROCHANTERION	-2.43	-7.63	23.94
LANDMARKS				
18	R GLUTEAL FOLD	-11.39	1.02	9.81
54	RIGHT ASIS	5.67	-1.45	30.39
57	R TROCHANTERION	-2.43	-7.63	23.94
59	R LAT FEM CONDYL	1.09	-6.55	-17.31
61	R MED FEM CONDYL	.89	4.72	-19.27
63	RIGHT TIBIALE	2.00	2.99	-22.06
65	RIGHT FIBULARE	.64	-7.13	-21.55
ANATOMICAL SYSTEM ORIGIN				
0		-2.43	-7.63	23.94
AXES DEFINITION POINTS			SEGMENT R CALF	
63	RIGHT TIBIALE	4.20	4.15	13.08
69	RIGHT SPHYRION	4.93	3.09	-25.07
67	R LAT MALLEOLUS	-.06	-2.05	-24.98
69	RIGHT SPHYRION	4.93	3.09	-25.07
63	RIGHT TIBIALE	4.20	4.15	13.08
63	RIGHT TIBIALE	4.20	4.15	13.08
LANDMARKS				
59	R LAT FEM CONDYL	.99	-5.39	16.73
61	R MED FEM CONDYL	3.75	5.71	16.14
63	RIGHT TIBIALE	4.20	4.15	13.08
65	RIGHT FIBULARE	.19	-5.25	12.51
67	R LAT MALLEOLUS	-.06	-2.05	-24.98
69	RIGHT SPHYRION	4.93	3.09	-25.07
ANATOMICAL SYSTEM ORIGIN				
0		4.20	4.15	13.08

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT R FOOT	
71	R METATARSAL I	7.69	3.95	-1.35
73	R METATARSAL V	5.66	-4.93	1.36
32	R POS CALCANEUS	-10.58	-1.74	-2.41
75	RIGHT TOE II	14.10	-.45	-.06
32	R POS CALCANEUS	-10.58	-1.74	-2.41
71	R METATARSAL I	7.69	3.95	-1.35
LANDMARKS				
32	R POS CALCANEUS	-10.58	-1.74	-2.41
67	R LAT MALLEOLUS	-7.30	-.84	4.39
69	RIGHT SPHYRION	-4.06	4.60	1.04
71	R METATARSAL I	7.69	3.95	-1.35
73	R METATARSAL V	5.66	-4.93	1.36
75	RIGHT TOE II	14.10	-.45	.06
ANATOMICAL SYSTEM ORIGIN				
0		7.78	-.49	.10
AXES DEFINITION POINTS			SEGMENT L FLAP	
56	L TROCHANTERION	4.99	8.46	2.22
58	L LAT FEM CONDYL	-3.16	-2.29	-36.01
60	L MED FEM CONDYL	-6.64	-13.07	-34.02
58	L LAT FEM CONDYL	-3.16	-2.29	-36.01
56	L TROCHANTERION	4.99	8.46	2.22
56	L TROCHANTERION	4.99	8.46	2.22
LANDMARKS				
17	L GLUTEAL FOLD	-9.35	-.97	-7.04
53	LEFT ASIS	11.88	2.90	9.25
55	SYMPHYSION	10.26	-10.89	4.53
56	L TROCHANTERION	4.99	8.46	2.22
ANATOMICAL SYSTEM ORIGIN				
0		4.99	8.46	2.22

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L THI-F	
56	L TROCHANTERION	-.22	8.08	23.21
58	L LAT FEM CONDYL	2.45	5.67	-17.17
60	L MED FEM CONDYL	-.21	-5.24	-19.14
58	L LAT FEM CONDYL	2.45	5.67	-17.17
56	L TROCHANTERION	-.22	8.08	23.21
56	L TROCHANTERION	-.22	8.08	23.21
LANDMARKS				
17	L GLUTEAL FOLD	-10.87	.39	8.79
53	LEFT ASIS	5.17	1.36	30.54
56	L TROCHANTERION	-.22	8.08	23.21
58	L LAT FEM CONDYL	2.45	5.67	-17.17
60	L MED FEM CONDYL	-.21	-5.24	-19.14
62	LEFT TIBIALE	2.04	-3.63	-21.77
64	LEFT FIBULARE	1.34	6.74	-22.04
ANATOMICAL SYSTEM ORIGIN				
0		-.22	8.08	23.21
AXES DEFINITION POINTS			SEGMENT L CALF	
62	LEFT TIBIALE	3.79	-4.54	13.16
68	LEFT SPHYRION	5.07	-3.33	-24.73
66	L LAT MALLEOLUS	1.23	2.17	-24.84
68	LEFT SPHYRION	5.07	-3.33	-24.73
62	LEFT TIBIALE	3.79	-4.54	13.16
62	LEFT TIBIALE	3.79	-4.54	13.16
LANDMARKS				
58	L LAT FEM CONDYL	2.58	5.13	16.69
60	L MED FEM CONDYL	2.60	-6.25	16.36
62	LEFT TIBIALE	3.79	-4.54	13.16
64	LEFT FIBULARE	.26	5.17	12.10
66	L LAT MALLEOLUS	1.23	2.17	-24.84
68	LEFT SPHYRION	5.07	-3.33	-24.73
ANATOMICAL SYSTEM ORIGIN				
0		3.79	-4.54	13.16

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L FOOT	
70	L METATARSAL I	7.29	-3.98	-1.23
72	L METATARSAL V	5.40	5.06	1.30
31	L POS CALCANEUS	-10.70	1.21	-2.57
74	LEFT TOE II	13.79	.10	-.73
31	L POS CALCANEUS	-10.70	1.21	-2.57
70	L METATARSAL I	7.29	-3.98	-1.23
LANDMARKS				
31	L POS CALCANEUS	-10.70	1.21	-2.57
66	L LAT MALLEOLUS	-6.73	.98	4.62
68	LEFT SPHYRION	-3.51	-4.34	1.94
70	L METATARSAL I	7.29	-3.98	-1.23
72	L METATARSAL V	5.40	5.06	1.30
74	LEFT TOE II	13.79	.10	-.73
ANATOMICAL SYSTEM ORIGIN				
0		7.37	.04	.05
AXES DEFINITION POINTS			SEGMENT R FARM+H	
20	R ULNAR STYLOID	-2.07	2.10	-8.71
22	R RADIAL STYLOID	-1.17	-2.75	-9.43
16	RIGHT RADIALE	-2.61	-1.69	15.42
20	R ULNAR STYLOID	-2.07	2.10	-8.71
16	RIGHT RADIALE	-2.61	-1.69	15.42
16	RIGHT RADIALE	-2.61	-1.69	15.42
LANDMARKS				
10	R MED HUM EPICON	2.35	3.84	17.06
12	R LAT HUM EPICON	-2.58	-2.64	17.20
14	RIGHT OLECRANON	-2.39	2.24	18.37
16	RIGHT RADIALE	-2.61	-1.69	15.42
20	R ULNAR STYLOID	-2.07	2.10	-8.71
22	R RADIAL STYLOID	-1.17	-2.75	-9.43
24	R METACARPALE II	-.61	-3.22	-17.72
26	R METACARPALEIII	-1.61	.13	-18.22
28	R METACARPALE V	-.80	4.63	-15.97
30	RIGHT DACTYLION	-.32	1.96	-20.02
ANATOMICAL SYSTEM ORIGIN				
0		-2.61	-1.69	15.42

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L FARM+H	
19	L ULNAR STYLOID	-1.45	-2.58	-8.69
21	L RADIAL STYLOID	-.49	2.98	-10.06
15	LEFT RADIALE	-2.37	1.06	15.14
19	L ULNAR STYLOID	-1.45	-2.58	-8.69
15	LEFT RADIALE	-2.37	1.06	15.14
15	LEFT RADIALE	-2.37	1.06	15.14
LANDMARKS				
9	L MED HUM EPICON	1.98	-4.21	17.00
11	L LAT HUM EPICON	-2.72	1.98	16.98
13	LEFT OLECRANON	-2.33	-2.44	17.61
15	LEFT RADIALE	-2.37	1.06	15.14
19	L ULNAR STYLOID	-1.45	-2.58	-8.69
21	L RADIAL STYLOID	-.49	2.98	-10.06
23	L METACARPALE II	-.02	3.31	-18.55
25	L METACARPALEIII	-1.03	.03	-18.71
27	L METACARPALE V	-.00	-4.52	-16.13
29	LEFT DACTYLION	-.87	-2.09	-28.29
ANATOMICAL SYSTEM ORIGIN				
0		-2.37	1.06	15.14
AXES DEFINITION POINTS			SEGMENT R THIGH	
57	R TROCHANTERION	1.49	-8.01	16.47
59	R LAT FEM CONDYL	-.01	-6.55	-24.89
61	R MED FEM CONDYL	-1.43	4.67	-26.67
59	R LAT FEM CONDYL	-.01	-6.55	-24.89
57	R TROCHANTERION	1.49	-8.01	16.47
57	R TROCHANTERION	1.49	-8.01	16.47
LANDMARKS				
18	R GLUTEAL FOLD	-9.81	-.16	3.60
54	RIGHT ASIS	9.72	-1.14	22.00
55	SYMPHYSION	10.38	11.77	13.30
57	R TROCHANTERION	1.49	-8.01	16.47
59	R LAT FEM CONDYL	-.01	-6.55	-24.89
61	R MED FEM CONDYL	-1.43	4.67	-26.67
63	RIGHT TIBIALE	-.51	3.05	-29.59
65	RIGHT FIBULARE	-.90	-7.16	-29.05
ANATOMICAL SYSTEM ORIGIN				
0		1.49	-8.01	16.47

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L THIGH	
56	L TROCHANTERION	3.32	7.78	16.11
58	L LAT FEM CONDYL	.64	6.00	-24.30
60	L MED FEM CONDYL	-2.24	-4.80	-26.07
58	L LAT FEM CONDYL	.64	6.00	-24.30
56	L TROCHANTERION	3.32	7.78	16.11
56	L TROCHANTERION	3.32	7.78	16.11
LANDMARKS				
17	L GLUTEAL FOLD	-9.12	.27	3.10
53	LEFT ASIS	9.65	.97	22.55
55	SYMPHYSION	9.54	-11.37	14.64
56	L TROCHANTERION	3.32	7.78	16.11
58	L LAT FEM CONDYL	.64	6.00	-24.30
60	L MED FEM CONDYL	-2.24	-4.80	-26.07
62	LEFT TIBIALE	-.36	-3.22	-28.96
64	LEFT FIBULARE	-1.11	7.15	-28.96
ANATOMICAL SYSTEM ORIGIN				
0		3.32	7.78	16.11

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT TORSO	
53	LEFT ASIS	8.32	12.82	-21.29
54	RIGHT ASIS	8.35	-12.53	-21.11
55	SYMPHYSION	9.78	.64	-29.31
53	LEFT ASIS	8.32	12.82	-21.29
54	RIGHT ASIS	8.35	-12.53	-21.11
8	POS SUP ILIAC MS	-9.75	.06	-14.38
LANDMARKS				
2	CERVICALE	-4.55	-.36	31.84
3	LEFT ACROMIALE	-4.28	18.38	24.39
4	RIGHT ACROMIALE	-2.46	-18.94	23.54
5	LEFT POS SCYE	-9.51	14.94	13.47
6	RIGHT POS SCYE	-7.89	-15.93	12.73
7	10TH RIBMIDSPINE	-7.65	.39	-7.35
8	POS SUP ILIAC MS	-9.75	.06	-14.38
42	LEFT CLAVICALE	5.36	2.79	26.85
43	RIGHT CLAVICALE	5.63	-2.69	26.69
44	SUPRASTERNALE	6.27	.13	25.53
45	LEFT ANT SCYE	2.39	15.79	12.59
46	RIGHT ANT SCYE	3.91	-15.47	12.22
49	LEFT 10TH RIB	-.11	13.03	-6.51
50	RIGHT 10TH RIB	-.10	-12.78	-7.02
51	L ILIOCRISTALE	-.06	15.31	-10.69
52	R ILIOCRISTALE	.19	-14.29	-9.65
53	LEFT ASIS	8.32	12.82	-21.29
54	RIGHT ASIS	8.35	-12.53	-21.11
55	SYMPHYSION	9.78	.64	-29.31
56	L TROCHANTERION	-.07	18.08	-26.76
57	R TROCHANTERION	-1.04	-18.17	-26.19
ANATOMICAL SYSTEM ORIGIN				
0		8.33	.03	-21.20

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT	TOT BODY
53	LEFT ASIS	11.01	12.27	-.03
54	RIGHT ASIS	9.91	-13.06	.30
55	SYMPHYSION	12.50	-.07	-7.80
53	LEFT ASIS	11.01	12.27	-.03
54	RIGHT ASIS	9.91	-13.06	.30
8	POS SUP ILIAC MS	-8.11	.30	5.51
LANDMARKS				
1	NUCHALE	-8.60	.31	61.16
2	CERVICALE	-6.60	.32	52.00
3	LEFT ACROMIALE	-4.91	18.86	44.43
4	RIGHT ACROMIALE	-4.75	-18.42	44.06
5	LEFT POS SCYE	-9.46	15.59	33.15
6	RIGHT POS SCYE	-9.15	-15.32	32.82
7	10TH RIBMIDSPINE	-6.57	.72	12.60
8	POS SUP ILIAC MS	-8.11	.30	5.51
9	L MED HUM EPICON	2.43	19.15	13.01
10	R MED HUM EPICON	2.83	-18.73	11.65
11	L LAT HUM EPICON	-3.45	23.90	14.65
12	R LAT HUM EPICON	-3.39	-23.55	13.74
13	LEFT OLECRANON	-2.19	19.70	13.50
14	RIGHT OLECRANON	-2.25	-18.79	12.61
15	LEFT RADIALE	-2.77	23.95	12.85
16	RIGHT RADIALE	-3.04	-23.57	11.76
17	L GLUTEAL FOLD	-8.30	8.10	-10.50
18	R GLUTEAL FOLD	-9.19	-8.33	-17.09
19	L ULNAR STYLOID	.86	31.47	-9.79
20	R ULNAR STYLOID	.72	-31.80	-10.95
21	L RADIAL STYLOID	.73	37.14	-8.52
22	R RADIAL STYLOID	.50	-36.55	-9.20
23	L METACARPALE II	1.81	41.27	-15.80
24	R METACARPALE II	1.83	-41.00	-16.12
25	L METACARPALEIII	.76	38.17	-17.70
26	R METACARPALEIII	1.65	-38.19	-18.25
27	L METACARPALE V	3.30	33.30	-17.80
28	R METACARPALE V	3.97	-33.44	-17.99
29	LEFT DACTYLION	2.94	40.71	-26.97
30	RIGHT DACTYLION	4.26	-41.46	-27.30
31	L POS CALCANEUS	-6.26	13.47	-94.24
32	R POS CALCANEUS	-7.26	-11.70	-94.39
33	HEAD CIRC	8.25	-.09	70.83
34	SELLION	8.95	.00	67.16

TABLE # 7 (CONTINUED) SUBJECT 11 SEGMENT PA AXES

SEGMENT LANDMARKS AND ANATOMICAL SYS. ORIGIN
WITH RESPECT TO SEGMENT PA AXES

#		X	Y	Z
35	L INFRAORBITALE	7.51	4.10	65.44
36	R INFRAORBITALE	7.39	-.45	65.23
37	LEFT TRAGION	.26	7.27	63.71
38	RIGHT TRAGION	.01	-7.05	63.61
39	LEFT GONION	1.52	5.60	58.01
40	RIGHT GONION	1.23	-5.51	58.01
41	MID THYROID CART	4.03	.22	51.03
42	LEFT CLAVICALE	3.73	2.98	47.80
43	RIGHT CLAVICALE	3.77	-2.50	47.71
44	SUPRASTERNALE	4.62	.27	46.59
45	LEFT ANT SCYE	2.50	15.92	33.23
46	RIGHT ANT SCYE	2.66	-15.38	33.27
47	LEFT BUSTPOINT	15.39	9.01	30.47
48	RIGHT BUSTPOINT	15.61	-9.29	30.11
49	LEFT 10TH RIB	1.43	13.03	14.01
50	RIGHT 10TH RIB	.35	-12.76	13.74
51	L ILIOCRISTALE	1.92	15.25	9.04
52	R ILIOCRISTALE	.70	-14.31	11.16
53	LEFT ASIS	11.01	12.27	-.03
54	RIGHT ASIS	9.91	-13.06	.30
55	SYMPHYSION	12.58	-.07	-7.80
56	L TROCHANTERION	3.33	17.01	-6.21
57	R TROCHANTERION	.72	-18.35	-5.39
58	L LAT FEM CONDYL	-.96	14.07	-46.41
59	R LAT FEM CONDYL	-.42	-15.01	-46.65
60	L MED FEM CONDYL	-2.07	3.64	-47.93
61	R MED FEM CONDYL	-.00	-3.65	-47.97
62	LEFT TIBIALE	-.63	5.53	-50.92
63	RIGHT TIBIALE	.50	-5.27	-50.97
64	LEFT FIBULARE	-3.10	15.63	-50.99
65	RIGHT FIBULARE	-1.39	-15.31	-50.03
66	L LAT MALLEOLUS	-1.71	16.35	-88.04
67	R LAT MALLEOLUS	-3.60	-14.60	-88.39
68	LEFT SPHYRION	1.52	10.49	-88.47
69	RIGHT SPHYRION	.19	-8.55	-88.99
70	L METATARSAL I	12.00	9.50	-92.46
71	R METATARSAL I	11.63	-9.06	-92.61
72	L METATARSAL V	9.90	18.73	-93.93
73	R METATARSAL V	8.55	-17.07	-94.35
74	LEFT TOE II	18.32	13.50	-94.42
75	RIGHT TOE II	17.45	-14.10	-94.28
76	CROTCH SENSOR	5.73	-.03	-15.73
77	(42 + 43)/2	3.75	.24	47.76

ANATOMICAL SYSTEM ORIGIN

	X	Y	Z
0	10.45	-.51	.10

TABLE # 8 SUBJECT 11 TOTAL BODY PA AXES

SEGMENT CENTERS OF GRAVITY
WITH RESPECT TO TOTAL BODY PA AXES

SEG	X	Y	Z
HEAD	-.64	-.09	67.13
NECK	-.75	.12	55.85
THORAX	-.18	.19	31.11
ABDOMEN	2.40	.05	12.29
PELVIS	1.43	-.10	2.85
RU ARM	-2.03	-19.10	26.93
RF ARM	.73	-26.95	3.24
R HAND	3.00	-36.94	-14.74
LU ARM	-2.31	19.62	28.13
LF ARM	.45	27.50	4.46
L HAND	2.50	37.09	-14.54
R FLAP	-.02	-9.60	-10.55
R THI-F	.92	-9.45	-29.01
R CALF	-3.11	-11.81	-63.58
R FOOT	3.55	-12.40	-92.55
L FLAP	.37	9.27	-10.65
L THI-F	.72	9.31	-29.12
L CALF	-3.66	11.70	-63.57
L FOOT	4.66	13.57	-92.41
R FARM+H	1.39	-29.05	-1.97
L FARM+H	1.01	30.11	-.71
R THIGH	.54	-9.55	-21.52
L THIGH	.58	9.30	-22.05
TORSO	.44	.09	20.63
TOTAL BODY			
TOT BODY	0.00	0.00	0.00

TABLE # 9 SUBJECT 11 TOTAL BODY PA AXES

ORIGIN OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO TOTAL BODY PA AXES

SEG	X	Y	Z
HEAD	.14	.25	63.66
NECK	-6.68	.32	52.08
THORAX	-6.57	.72	12.68
ABDOMEN	.90	.39	13.08
PELVIS	10.45	-.51	.18
RU ARM	-4.75	-18.42	44.86
RF ARM	-3.04	-23.57	11.76
R HAND	2.65	-30.12	-16.84
LU ARM	-4.91	18.86	44.43
LF ARM	-2.77	23.95	12.85
L HAND	2.37	30.27	-16.30
R FLAP	.72	-10.35	-5.39
R THI-F	.72	-10.35	-5.39
R CALF	.50	-5.27	-50.97
R FOOT	11.19	-13.65	-93.43
L FLAP	3.33	17.01	-6.21
L THI-F	3.33	17.01	-6.21
L CALF	-.63	5.53	-50.92
L FOOT	11.99	13.60	-93.07
R FARM+H	-3.04	-23.57	11.76
L FARM+H	-2.77	23.95	12.85
R THIGH	.72	-10.35	-5.39
L THIGH	3.33	17.01	-6.21
TORSO	10.45	-.51	.18
TOTAL BODY			
TOT BODY	10.45	-.51	.18

TABLE # 10 SUBJECT 11 ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT HEAD	
37	LEFT TRAGION	.00	7.02	-.00
38	RIGHT TRAGION	.00	-7.31	-.00
36	R INFRAORBITALE	7.43	-.56	-.00
37	LEFT TRAGION	.00	7.02	-.00
38	RIGHT TRAGION	.00	-7.31	-.00
34	SELLION	9.36	.00	1.56
LANDMARKS				
1	NUCHALE	-9.07	-.11	-.59
34	SELLION	9.36	.00	1.56
36	R INFRAORBITALE	7.43	-.56	-.00
37	LEFT TRAGION	.00	7.02	-.00
38	RIGHT TRAGION	.00	-7.31	-.00
39	LEFT GONION	.05	5.41	-5.83
40	RIGHT GONION	-.02	-5.70	-5.73
CENTER OF GRAVITY				
0		-.02	-.33	3.56
AXES DEFINITION POINTS			SEGMENT NECK	
41	MID THYROID CART	9.99	.00	3.00
2	CERVICALE	.00	.00	.00
44	SUPRASTERNALE	12.51	.00	-.76
77	(42 + 43)/2	11.26	-.03	.00
2	CERVICALE	.00	.00	.00
2	CERVICALE	.00	.00	.00
LANDMARKS				
1	NUCHALE	-5.23	.06	7.77
2	CERVICALE	.00	.00	.00
39	LEFT GONION	5.30	5.58	8.58
40	RIGHT GONION	5.10	-5.69	8.63
41	MID THYROID CART	9.99	.00	3.00
42	LEFT CLAVICALE	11.21	2.71	-.00
43	RIGHT CLAVICALE	11.31	-2.77	.00
44	SUPRASTERNALE	12.51	.00	-.76
CENTER OF GRAVITY				
0		4.34	-.11	5.06

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT THORAX	
44	SUPRASTERNALE	11.29	.00	33.07
2	CERVICALE	.00	.00	39.31
7	10TH RIBMIDSPINE	.00	.00	.00
2	CERVICALE	.00	.00	39.31
7	10TH RIBMIDSPINE	.00	.00	.00
7	10TH RIBMIDSPINE	.00	.00	.00
LANDMARKS.				
2	CERVICALE	.00	.00	39.31
3	LEFT ACROMIALE	1.57	10.47	31.56
4	RIGHT ACROMIALE	2.09	-10.81	31.56
5	LEFT POS SCYE	-2.98	15.05	20.32
6	RIGHT POS SCYE	-2.37	-15.86	20.30
7	10TH RIBMIDSPINE	.00	.00	.00
42	LEFT CLAVICALE	10.37	2.71	35.07
43	RIGHT CLAVICALE	10.47	-2.77	35.03
44	SUPRASTERNALE	11.29	.00	33.07
45	LEFT ANT SCYE	8.98	15.49	20.37
46	RIGHT ANT SCYE	9.45	-15.79	20.72
49	LEFT 10TH RIB	7.89	12.41	1.10
50	RIGHT 10TH RIB	7.06	-13.40	1.17
CENTER OF GRAVITY				
0		6.45	-.20	18.41
AXES DEFINITION POINTS			SEGMENT ABDOMEN	
49	LEFT 10TH RIB	.00	12.65	.00
50	RIGHT 10TH RIB	.00	-13.16	.00
7	10TH RIBMIDSPINE	-7.57	.00	.00
49	LEFT 10TH RIB	.00	12.65	.00
50	RIGHT 10TH RIB	.00	-13.16	.00
7	10TH RIBMIDSPINE	-7.57	.00	.00
LANDMARKS				
7	10TH RIBMIDSPINE	-7.57	.00	.00
8	POS SUP ILIAC MS	-10.21	-.47	-6.04
49	LEFT 10TH RIB	.00	12.65	.00
50	RIGHT 10TH RIB	.00	-13.16	.00
51	L ILIOCRISTALE	-.27	14.04	-4.21
52	R ILIOCRISTALE	.00	-14.72	-2.61
CENTER OF GRAVITY				
0		1.24	-.29	-1.00

TABLE # 10 (CONTINUED) SUBJECT 11 ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT PELVIS	
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
55	SYMPHYSION	.00	.67	-8.23
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
8	POS SUP ILIAC MS	-16.60	-.00	9.90
LANDMARKS				
8	POS SUP ILIAC MS	-16.60	-.00	9.90
51	L ILIOCRISTALE	-6.38	15.21	11.93
52	R ILIOCRISTALE	-6.82	-14.39	12.71
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
55	SYMPHYSION	.00	.67	-8.23
56	L TROCHANTERION	-9.21	18.10	-3.87
57	R TROCHANTERION	-10.14	-18.15	-3.38
CENTER OF GRAVITY				
0		-8.26	-.01	4.11
AXES DEFINITION POINTS			SEGMENT RU ARM	
4	RIGHT ACROMIALE	.00	-.00	.00
10	R MED HUM EPICON	.00	8.00	-32.31
12	R LAT HUM EPICON	.00	-.00	-30.78
4	RIGHT ACROMIALE	.00	-.00	.00
12	R LAT HUM EPICON	.00	-.00	-30.78
4	RIGHT ACROMIALE	.00	-.00	.00
LANDMARKS				
4	RIGHT ACROMIALE	.00	-.00	.00
6	RIGHT POS SCYE	-6.90	-.60	-10.36
10	R MED HUM EPICON	.00	8.00	-32.31
12	R LAT HUM EPICON	.00	-.00	-30.78
14	RIGHT OLECRANON	-3.04	3.90	-31.15
16	RIGHT RADIALE	-.06	.40	-32.75
46	RIGHT ANT SCYE	.74	8.42	-10.45
CENTER OF GRAVITY				
0		-.37	2.86	-17.12

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT RF ARM	
20	R ULNAR STYLOID	.00	.00	-24.44
22	R RADIAL STYLOID	.00	-5.06	-24.40
16	RIGHT RADIALE	.00	.00	.00
20	R ULNAR STYLOID	.00	.00	-24.44
16	RIGHT RADIALE	.00	.00	.00
16	RIGHT RADIALE	.00	.00	.00
LANDMARKS				
10	R MED HUM EPICON	5.92	4.75	.63
12	R LAT HUM EPICON	-.05	-.65	1.90
14	RIGHT OLECRANON	1.04	4.23	2.20
16	RIGHT RADIALE	.00	.00	.00
20	R ULNAR STYLOID	.00	.00	-24.44
22	R RADIAL STYLOID	.00	-5.06	-24.40
CENTER OF GRAVITY				
0		2.32	-.21	-9.64
AXES DEFINITION POINTS			SEGMENT R HAND	
30	RIGHT DACTYLION	.00	-.25	-11.10
24	R METACARPALE II	.00	-3.07	-.00
28	R METACARPALE V	.00	5.00	-.00
24	R METACARPALE II	.00	-3.07	-.00
28	R METACARPALE V	.00	5.00	-.00
26	R METACARPALEIII	-1.24	-.00	-1.21
LANDMARKS				
20	R ULNAR STYLOID	-1.94	4.04	7.63
22	R RADIAL STYLOID	-.67	-.05	7.99
24	R METACARPALE II	.00	-3.07	-.00
26	R METACARPALEIII	-1.24	-.00	-1.21
28	R METACARPALE V	.00	5.00	-.00
30	RIGHT DACTYLION	.00	-.25	-11.10
CENTER OF GRAVITY				
0		.53	.71	2.26

TABLE # 10 (CONTINUED) SUBJECT 11 ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT LU ARM	
3	LEFT ACROMIALE	.00	-.00	.00
9	L MED HUM EPICON	.00	-7.70	-31.33
11	L LAT HUM EPICON	.00	-.00	-30.25
3	LEFT ACROMIALE	.00	-.00	.00
11	L LAT HUM EPICON	.00	-.00	-30.25
3	LEFT ACROMIALE	.00	-.00	.00
LANDMARKS				
3	LEFT ACROMIALE	.00	-.00	.00
5	LEFT POS SCYE	-7.19	.47	-10.33
9	L MED HUM EPICON	.00	-7.70	-31.33
11	L LAT HUM EPICON	.00	-.00	-30.25
13	LEFT OLECRANON	-2.46	-3.76	-30.65
15	LEFT RADIALE	.14	-.67	-32.06
45	LEFT ANT SCYE	.80	-8.35	-10.89
CENTER OF GRAVITY				
0		-.34	-2.60	-16.30
AXES DEFINITION POINTS			SEGMENT LF ARM	
19	L ULNAR STYLOID	.00	.00	-24.13
21	L RADIAL STYLOID	.00	5.70	-24.60
15	LEFT RADIALE	.00	.00	.00
19	L ULNAR STYLOID	.00	.00	-24.13
15	LEFT RADIALE	.00	.00	.00
15	LEFT RADIALE	.00	.00	.00
LANDMARKS				
9	L MED HUM EPICON	5.22	-4.70	.07
11	L LAT HUM EPICON	-.39	.61	1.79
13	LEFT OLECRANON	.73	-3.76	1.91
15	LEFT RADIALE	.00	.00	.00
19	L ULNAR STYLOID	.00	.00	-24.13
21	L RADIAL STYLOID	.00	5.70	-24.60
CENTER OF GRAVITY				
0		1.04	.66	-9.46

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L HAND	
29	LEFT DACTYLION	-.00	.01	-10.93
23	L METACARPALE II	-.00	3.00	.00
27	L METACARPALE V	-.00	-5.10	.00
23	L METACARPALE II	-.00	3.00	.00
27	L METACARPALE V	-.00	-5.10	.00
25	L METACARPALEIII	-1.72	.00	-1.26
LANDMARKS				
19	L ULNAR STYLOID	-2.04	-5.45	7.54
21	L RADIAL STYLOID	-1.10	.27	7.95
23	L METACARPALE II	-.00	3.00	.00
25	L METACARPALEIII	-1.72	.00	-1.26
27	L METACARPALE V	-.00	-5.10	.00
29	LEFT DACTYLION	-.00	.01	-10.93
CENTER OF GRAVITY				
0		.09	-.93	1.90
AXES DEFINITION POINTS			SEGMENT R FLAP	
57	R TROCHANTERION	.00	.00	.00
59	R LAT FEM CONDYL	.00	.00	-41.41
61	R MED FEM CONDYL	.00	11.23	-43.64
59	R LAT FEM CONDYL	.00	.00	-41.41
57	R TROCHANTERION	.00	.00	.00
57	R TROCHANTERION	.00	.00	.00
LANDMARKS				
18	R GLUTEAL FOLD	-9.06	8.62	-13.54
54	RIGHT ASIS	8.02	6.06	5.50
55	SYMPHYSION	11.30	10.44	-3.54
57	R TROCHANTERION	.00	.00	.00
CENTER OF GRAVITY				
0		-.07	8.19	-5.06

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT R THI-F	
57	R TROCHANTERION	.00	.00	.00
59	R LAT FEM CONDYL	.00	.00	-41.41
61	R MED FEM CONDYL	.00	11.23	-43.64
59	R LAT FEM CONDYL	.00	.00	-41.41
57	R TROCHANTERION	.00	.00	.00
57	R TROCHANTERION	.00	.00	.00
LANDMARKS				
10	R GLUTEAL FOLD	-9.86	8.62	-13.54
54	RIGHT ASIS	8.02	6.06	5.50
57	R TROCHANTERION	.00	.00	.00
59	R LAT FEM CONDYL	.00	.00	-41.41
61	R MED FEM CONDYL	.00	11.23	-43.64
63	RIGHT TIBIALE	.01	9.40	-46.47
65	RIGHT FIBULARE	-.03	-.66	-45.50
CENTER OF GRAVITY				
0		.61	6.99	-24.25
AXES DEFINITION POINTS			SEGMENT R CALF	
63	RIGHT TIBIALE	-.00	-.00	.00
69	RIGHT SPHYRION	-.00	-.00	-30.17
67	R LAT MALLEOLUS	-.00	-7.17	-30.12
69	RIGHT SPHYRION	-.00	-.00	-30.17
63	RIGHT TIBIALE	-.00	-.00	.00
63	RIGHT TIBIALE	-.00	-.00	.00
LANDMARKS				
59	R LAT FEM CONDYL	4.45	-9.10	3.45
61	R MED FEM CONDYL	-1.31	.70	3.11
63	RIGHT TIBIALE	-.00	-.00	.00
65	RIGHT FIBULARE	3.64	-9.53	-.75
67	R LAT MALLEOLUS	-.00	-7.17	-30.12
69	RIGHT SPHYRION	-.00	-.00	-30.17
CENTER OF GRAVITY				
0		-.56	-5.02	-13.10

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT R FOOT	
71	R METATARSAL I	.00	4.69	.00
73	R METATARSAL V	-2.23	-4.54	.00
32	R POS CALCANEUS	-18.58	-.00	.00
75	RIGHT TOE II	6.22	-.00	-1.19
32	R POS CALCANEUS	-18.58	-.00	.00
71	R METATARSAL I	.00	4.69	.00
LANDMARKS				
32	R POS CALCANEUS	-18.58	-.00	.00
67	R LAT MALLEOLUS	-14.33	-1.44	6.14
69	RIGHT SPHYRION	-11.23	4.74	4.26
71	R METATARSAL I	.00	4.69	.00
73	R METATARSAL V	-2.23	-4.54	.00
75	RIGHT TOE II	6.22	-.00	-1.19
CENTER OF GRAVITY				
0		-7.67	.66	1.18
AXES DEFINITION POINTS			SEGMENT L FLAP	
56	L TROCHANTERION	-.00	.00	.00
58	L LAT FEM CONDYL	-.00	.00	-40.54
60	L MED FEM CONDYL	-.00	-11.13	-42.97
58	L LAT FEM CONDYL	-.00	.00	-40.54
56	L TROCHANTERION	-.00	.00	.00
56	L TROCHANTERION	-.00	.00	.00
LANDMARKS				
17	L GLUTEAL FOLD	-9.49	-9.54	-14.12
53	LEFT ASIS	7.46	-5.42	6.54
55	SYMPHYSION	10.82	-16.94	-1.89
56	L TROCHANTERION	-.00	.00	.00
CENTER OF GRAVITY				
0		-1.78	-8.35	-5.34

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L THI-F	
56	L TROCHANTERION	-.00	.00	.00
58	L LAT FEM CONDYL	-.00	.00	-40.54
60	L MED FEM CONDYL	-.00	-11.13	-42.97
58	L LAT FEM CONDYL	-.00	.00	-40.54
56	L TROCHANTERION	-.00	.00	.00
56	L TROCHANTERION	-.00	.00	.00
LANDMARKS				
17	L GLUTEAL FOLD	-9.49	-9.54	-14.12
53	LEFT ASIS	7.46	-5.42	6.54
56	L TROCHANTERION	-.00	.00	.00
58	L LAT FEM CONDYL	-.00	.00	-40.54
60	L MED FEM CONDYL	-.00	-11.13	-42.97
62	LEFT TIBIALE	1.56	-8.90	-45.65
64	LEFT FIBULARE	-1.72	.95	-45.25
CENTER OF GRAVITY				
0		.41	-6.00	-23.61
AXES DEFINITION POINTS			SEGMENT L CALF	
62	LEFT TIBIALE	.00	.00	.00
68	LEFT SPHYRION	.00	.00	-37.93
66	L LAT MALLEOLUS	.00	6.70	-30.09
68	LEFT SPHYRION	.00	.00	-37.93
62	LEFT TIBIALE	.00	.00	.00
62	LEFT TIBIALE	.00	.00	.00
LANDMARKS				
58	L LAT FEM CONDYL	4.64	0.65	3.26
60	L MED FEM CONDYL	-1.01	-.69	3.29
62	LEFT TIBIALE	.00	.00	.00
64	LEFT FIBULARE	2.62	9.90	-1.25
66	L LAT MALLEOLUS	.00	6.70	-30.09
68	LEFT SPHYRION	.00	.00	-37.93
CENTER OF GRAVITY				
0		-1.11	5.01	-13.17

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L FOOT	
70	L METATARSAL I	.00	-4.22	.00
72	L METATARSAL V	-2.00	5.13	.00
31	L POS CALCANEUS	-18.29	.00	.00
74	LEFT TOE II	6.22	.00	-1.70
31	L POS CALCANEUS	-18.29	.00	.00
70	L METATARSAL I	.00	-4.22	.00
LANDMARKS				
31	L POS CALCANEUS	-18.29	.00	.00
66	L LAT MALLEOLUS	-13.32	1.95	6.24
68	LEFT SPHYRION	-10.19	-3.80	4.77
70	L METATARSAL I	.00	-4.22	.00
72	L METATARSAL V	-2.00	5.13	.00
74	LEFT TOE II	6.22	.00	-1.70
CENTER OF GRAVITY				
0		-7.20	-.19	1.11
AXES DEFINITION POINTS			SEGMENT R FARM+H	
20	R ULNAR STYLOID	.00	.00	-24.44
22	R RADIAL STYLOID	.00	-5.06	-24.40
16	RIGHT RADIALE	.00	.00	.00
20	R ULNAR STYLOID	.00	.00	-24.44
16	RIGHT RADIALE	.00	.00	.00
16	RIGHT RADIALE	.00	.09	.00
LANDMARKS				
10	R MED HUM EPICON	5.92	4.75	.63
12	R LAT HUM EPICON	-.05	-.65	1.90
14	RIGHT OLECRANON	1.04	4.23	2.20
16	RIGHT RADIALE	.00	.00	.00
20	R ULNAR STYLOID	.00	.00	-24.44
22	R RADIAL STYLOID	.00	-5.06	-24.40
24	R METACARPALE II	.05	-6.00	-32.52
26	R METACARPALEIII	-.37	-3.53	-33.52
28	R METACARPALE V	2.09	.91	-32.04
30	RIGHT DACTYLION	.72	-3.46	-43.51
CENTER OF GRAVITY				
0		2.09	-1.16	-15.55

TABLE # 10 (CONTINUED) SUBJECT 11 ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L FARM+H	
19	L ULNAR STYLOID	.00	.00	-24.13
21	L RADIAL STYLOID	.00	5.70	-24.60
15	LEFT RADIALE	.00	.00	.00
19	L ULNAR STYLOID	.00	.00	-24.13
15	LEFT RADIALE	.00	.00	.00
15	LEFT RADIALE	.00	.00	.00
LANDMARKS				
9	L MED HUM EPICON	5.22	-4.70	.87
11	L LAT HUM EPICON	-.39	.61	1.79
13	LEFT OLECRANON	.73	-3.76	1.91
15	LEFT RADIALE	.00	.00	.00
19	L ULNAR STYLOID	.00	.00	-24.13
21	L RADIAL STYLOID	.00	5.70	-24.60
23	L METACARPALE II	-.12	7.39	-33.03
25	L METACARPALEIII	-1.40	3.92	-33.62
27	L METACARPALE V	1.27	-.59	-31.83
29	LEFT DACTYLION	-.71	3.38	-43.44
CENTER OF GRAVITY				
0		1.56	1.52	-15.21
AXES DEFINITION POINTS			SEGMENT R THIGH	
57	R TROCHANTERION	.00	.00	.00
59	R LAT FEM CONDYL	.00	.00	-41.41
61	R MED FEM CONDYL	.00	11.23	-43.64
59	R LAT FEM CONDYL	.00	.00	-41.41
57	R TROCHANTERION	.00	.00	.00
57	R TROCHANTERION	.00	.00	.00
LANDMARKS				
18	R GLUTEAL FOLD	-9.86	8.62	-13.54
54	RIGHT ASIS	8.82	6.06	5.58
55	SYMPHYSION	11.38	10.44	-3.54
57	R TROCHANTERION	.00	.00	.00
59	R LAT FEM CONDYL	.00	.00	-41.41
61	R MED FEM CONDYL	.00	11.23	-43.64
63	RIGHT TIBIALE	.81	9.40	-46.47
65	RIGHT FIBULARE	-.83	-.66	-45.58
CENTER OF GRAVITY				
0		.01	7.40	-16.79

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT L THIGH	
56	L TROCHANTERION	-.00	.00	.00
58	L LAT FEM CONDYL	-.00	.00	-40.54
60	L MED FEM CONDYL	-.00	-11.13	-42.97
58	L LAT FEM CONDYL	-.00	.00	-40.54
56	L TROCHANTERION	-.00	.00	.00
56	L TROCHANTERION	-.00	.00	.00
LANDMARKS				
17	L GLUTEAL FOLD	-9.49	-9.54	-14.12
53	LEFT ASIS	7.46	-5.42	6.54
55	SYMPHYSION	10.82	-16.94	-1.89
56	L TROCHANTERION	-.00	.00	.00
58	L LAT FEM CONDYL	-.00	.00	-40.54
60	L MED FEM CONDYL	-.00	-11.13	-42.97
62	LEFT TIBIALE	1.56	-8.90	-45.65
64	LEFT FIBULARE	-1.72	.95	-45.25
CENTER OF GRAVITY				
0		-.43	-7.39	-16.62

TABLE # 10 (CONTINUED) SUBJECT 11 ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT TORSO	
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
55	SYMPHYSION	.00	.67	-8.23
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
8	POS SUP ILIAC MS	-16.60	-.00	9.90
LANDMARKS				
2	CERVICALE	-3.36	-.75	54.40
3	LEFT ACROMIALE	-4.29	17.96	47.21
4	RIGHT ACROMIALE	-2.01	-19.27	45.01
5	LEFT POS SCYE	-11.44	14.60	37.37
6	RIGHT POS SCYE	-10.05	-16.10	36.15
7	10TH RIBMIDSPINE	-13.30	.20	16.45
8	POS SUP ILIAC MS	-16.60	-.00	9.90
42	LEFT CLAVICALE	5.53	2.42	47.05
43	RIGHT CLAVICALE	5.75	-3.05	47.60
44	SUPRASTERNALE	6.10	-.23	46.37
45	LEFT ANT SCYE	.12	15.53	34.41
46	RIGHT ANT SCYE	1.40	-15.72	33.50
49	LEFT 10TH RIB	-5.70	12.91	16.03
50	RIGHT 10TH RIB	-5.03	-12.90	15.36
51	L ILIOCRISTALE	-6.30	15.21	11.93
52	R ILIOCRISTALE	-6.02	-14.39	12.71
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
55	SYMPHYSION	.00	.67	-8.23
56	L TROCHANTERION	-9.21	10.10	-3.07
57	R TROCHANTERION	-10.14	-10.15	-3.30
CENTER OF GRAVITY				
0		-4.40	-.17	22.34

TABLE # 10 (CONTINUED)   SUBJECT 11   ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
AXES DEFINITION POINTS			SEGMENT	TOT BODY
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
55	SYMPHYSION	.00	.67	-8.23
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
8	POS SUP ILIAC MS	-16.60	-.00	9.90
LANDMARKS				
1	NUCHALE	-2.88	-1.00	63.82
2	CERVICALE	-3.36	-.75	54.40
3	LEFT ACROMIALE	-4.29	17.96	47.21
4	RIGHT ACROMIALE	-2.81	-19.27	45.81
5	LEFT POS SCYE	-11.44	14.60	37.37
6	RIGHT POS SCYE	-10.05	-16.10	36.15
7	10TH RIBMIDSPINE	-13.30	.20	16.45
8	POS SUP ILIAC MS	-16.60	-.00	9.90
9	L MED HUM EPICON	-5.23	19.00	14.90
10	R MED HUM EPICON	-3.74	-18.71	12.54
11	L LAT HUM EPICON	-10.67	23.62	18.10
12	R LAT HUM EPICON	-9.04	-23.84	16.02
13	LEFT OLECRANON	-9.57	19.50	16.72
14	RIGHT OLECRANON	-8.40	-19.01	14.76
15	LEFT RADIALE	-10.47	23.66	16.27
16	RIGHT RADIALE	-9.20	-23.01	14.01
17	L GLUTEAL FOLD	-23.21	8.09	-13.05
18	R GLUTEAL FOLD	-23.29	-8.30	-12.60
19	L ULNAR STYLOID	-13.03	31.69	-6.34
20	R ULNAR STYLOID	-11.06	-31.50	-9.11
21	L RADIAL STYLOID	-13.05	37.33	-4.92
22	R RADIAL STYLOID	-10.56	-36.28	-7.52
23	L METACARPALE II	-14.03	41.62	-12.20
24	R METACARPALE II	-10.95	-40.55	-14.65
25	L METACARPALEIII	-15.40	38.50	-13.70
26	R METACARPALEIII	-11.77	-37.72	-16.59
27	L METACARPALE V	-12.59	33.74	-13.00
28	R METACARPALE V	-9.65	-32.00	-16.00
29	LEFT DACTYLION	-15.76	41.29	-23.23
30	RIGHT DACTYLION	-11.45	-40.72	-26.17
31	L POS CALCANEUS	-40.77	14.77	-86.66
32	R POS CALCANEUS	-40.82	-10.42	-87.22
33	HEAD CIRC	15.89	-.02	60.87
34	SELLION	15.62	-.56	65.16

TABLE # 10 (CONTINUED) SUBJECT 11 ANATOMICAL AXES

SEGMENT LANDMARKS AND CENTER OF GRAVITY
WITH RESPECT TO ANATOMICAL AXES

#		X	Y	Z
35	L INFRAORBITALE	13.63	3.50	63.97
36	R INFRAORBITALE	13.64	-1.12	63.67
37	LEFT TRAGION	6.07	6.30	64.22
38	RIGHT TRAGION	6.35	-8.02	63.80
39	LEFT GONION	5.89	4.86	58.35
40	RIGHT GONION	6.04	-6.33	58.13
41	MID THYROID CART	6.95	-.39	51.59
42	LEFT CLAVICALE	5.53	2.42	47.85
43	RIGHT CLAVICALE	5.75	-3.05	47.60
44	SUPRASTERNALE	6.18	-.23	46.37
45	LEFT ANT SCYE	.12	15.53	34.41
46	RIGHT ANT SCYE	1.48	-15.72	33.58
47	LEFT BUSTPOINT	12.11	10.03	28.30
48	RIGHT BUSTPOINT	12.95	-9.03	27.39
49	LEFT 10TH RIB	-5.70	12.91	16.03
50	RIGHT 10TH RIB	-5.83	-12.90	15.36
51	L ILIOCRISTALE	-6.38	15.21	11.93
52	R ILIOCRISTALE	-6.02	-14.39	12.71
53	LEFT ASIS	.00	12.80	.00
54	RIGHT ASIS	.00	-12.56	.00
55	SYMPHYSION	.00	.67	-8.23
56	L TROCHANTERION	-9.21	18.10	-3.87
57	R TROCHANTERION	-10.14	-18.15	-3.38
58	L LAT FEM CONDYL	-23.50	15.63	-41.73
59	R LAT FEM CONDYL	-21.90	-14.20	-42.89
60	L MED FEM CONDYL	-24.53	4.30	-43.21
61	R MED FEM CONDYL	-22.34	-2.81	-43.96
62	LEFT TIBIALE	-23.90	6.38	-46.42
63	RIGHT TIBIALE	-22.40	-4.35	-47.06
64	LEFT FIBULARE	-26.76	16.36	-45.59
65	RIGHT FIBULARE	-23.89	-14.47	-46.70
66	L LAT MALLEOLUS	-34.90	17.74	-81.74
67	R LAT MALLEOLUS	-35.64	-13.25	-82.42
68	LEFT SPHYRION	-31.67	12.04	-83.13
69	RIGHT SPHYRION	-32.36	-7.03	-83.01
70	L METATARSAL I	-22.52	11.57	-89.60
71	R METATARSAL I	-22.21	-6.98	-90.23
72	L METATARSAL V	-25.28	20.72	-90.33
73	R METATARSAL V	-25.30	-15.89	-91.36
74	LEFT TOE II	-17.07	15.00	-93.00
75	RIGHT TOE II	-16.03	-11.74	-93.46
76	CROTCH SENSOR	-8.64	.53	-14.16
77	(42 + 43)/2	5.64	-.31	47.73
CENTER OF GRAVITY				
0		-10.16	.06	2.58

TABLE # 11 SUBJECT 11 TOTAL BODY ANATO AXES

SEGMENT CENTERS OF GRAVITY
WITH RESPECT TO TOTAL BODY ANATOMICAL AXES

SEG	X	Y	Z
HEAD	6.35	-1.15	67.56
NECK	3.15	-.74	55.92
THORAX	-2.40	-.26	32.63
ABDOMEN	-4.71	.02	13.70
PELVIS	-8.26	-.01	4.11
RU ARM	-4.52	-19.63	20.54
RF ARM	-7.61	-26.89	4.72
R HAND	-9.62	-36.47	-13.50
LU ARM	-5.97	19.10	30.01
LF ARM	-9.64	27.40	7.43
L HAND	-12.87	37.46	-11.20
R FLAP	-12.50	-9.44	-7.95
R THI-F	-16.32	-8.87	-26.03
R CALF	-20.97	-10.05	-58.40
R FOOT	-29.80	-10.67	-88.20
L FLAP	-12.80	9.51	-7.64
L THI-F	-17.26	9.86	-25.59
L CALF	-30.37	12.70	-57.71
L FOOT	-29.76	15.32	-87.66
R FARM+H	-8.19	-29.66	-.56
L FARM+H	-10.52	30.20	2.36
R THIGH	-14.77	-9.10	-10.70
L THIGH	-15.50	9.73	-10.72
TORSO	-4.40	-.17	22.34

TOTAL BODY

TOT BODY	-10.16	.06	2.50

TABLE # 12 SUBJECT 11 TOTAL BODY ANATO AXES

ORIGIN OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO TOTAL BODY ANATOMICAL AXES

SEG	X	Y	Z
HEAD	6.20	-.71	64.82
NECK	-3.36	-.75	54.40
THORAX	-13.30	.28	16.45
ABDOMEN	-5.77	.26	15.70
PELVIS	0.00	0.00	0.00
RU ARM	-2.81	-19.27	45.01
RF ARM	-9.20	-23.81	14.01
R HAND	-10.45	-37.63	-15.47
LU ARM	-4.29	17.96	47.21
LF ARM	-10.47	23.66	16.27
L HAND	-13.49	30.65	-12.03
R FLAP	-10.14	-10.15	-3.38
R THI-F	-10.14	-10.15	-3.38
R CALF	-22.40	-4.35	-47.06
R FOOT	-22.60	-11.58	-91.04
L FLAP	-9.21	10.10	-3.87
L THI-F	-9.21	10.10	-3.87
L CALF	-23.90	6.30	-46.42
L FOOT	-22.84	15.76	-90.15
R FARM+H	-9.20	-23.81	14.01
L FARM+H	-10.47	23.66	16.27
R THIGH	-10.14	-10.15	-3.38
L THIGH	-9.21	10.10	-3.87
TORSO	0.00	0.00	0.00
TOTAL BODY			
TOT BODY	0.00	0.00	0.00

TABLE # 13 SUBJECT 11 SEGMENT PA AXES

DIRECTION COSINES (ANGLES) OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO SEGMENT PA AXES
(RA) = [DAG] [DGP] (RP)

SEGMENTS			
HEAD	.86358(30.3)	-.12035(96.9)	-.48963(119.3)
	.10250(84.1)	.99272(6.9)	-.06321(93.6)
	.49368(60.4)	.00440(89.7)	.86964(29.6)
NECK	.98567(9.7)	-.08174(94.7)	.14755(81.5)
	.08261(85.3)	.99658(4.7)	.00024(90.0)
	-.14707(98.5)	.01195(89.3)	.98905(8.5)
THORAX	.96737(14.7)	.02094(88.8)	-.25251(104.6)
	-.00944(90.5)	.99887(2.7)	.04668(87.3)
	.25320(75.3)	-.04277(92.5)	.96647(14.9)
ABDOMEN	.99259(7.0)	.00116(89.9)	.12149(83.0)
	-.00173(90.1)	.99999(.3)	.00459(89.7)
	-.12149(97.0)	-.00477(90.3)	.99258(7.0)
PELVIS	.99445(6.0)	.04334(87.5)	-.09583(95.5)
	-.04372(92.5)	.99904(2.5)	-.00187(90.1)
	.09566(84.5)	.00605(89.7)	.99540(5.5)
RU ARM	.73441(42.7)	-.67794(132.7)	-.03224(91.8)
	.66970(48.0)	.73156(43.0)	-.12770(97.3)
	.11021(83.7)	.07225(85.9)	.99128(7.6)
RF ARM	.92953(21.6)	.35709(69.1)	.09202(84.7)
	-.36705(111.5)	.91994(23.1)	.13782(82.1)
	-.03544(92.0)	-.16189(99.3)	.98617(9.5)
R HAND	.96858(14.4)	-.24796(104.4)	-.01922(91.1)
	.24740(75.7)	.95325(17.6)	.17341(80.0)
	-.02460(91.4)	-.17272(99.9)	.98466(10.0)
LU ARM	.81525(35.4)	.57703(54.8)	-.04908(92.8)
	-.56916(124.7)	.81399(35.5)	.11600(83.3)
	.10687(83.9)	-.06674(93.8)	.99203(7.2)
LF ARM	.94560(19.0)	-.30980(108.0)	.09930(84.3)
	.32154(71.2)	.93642(20.5)	-.14047(98.1)
	-.04947(92.8)	.16476(80.5)	.98509(9.9)
L HAND	.97966(11.6)	.19426(78.8)	-.05032(92.9)
	-.20062(101.6)	.95369(17.5)	-.22410(103.0)
	.00445(89.7)	.22964(76.7)	.97327(13.3)
R FLAP	.98444(10.1)	.16794(80.3)	-.05170(93.0)
	-.14436(98.3)	.94079(19.8)	.30672(72.1)
	.10023(84.2)	-.29447(107.1)	.95039(18.1)
R THI-F	.99581(5.2)	.03184(88.2)	.08575(85.1)
	-.03395(91.9)	.99915(2.4)	.02326(88.7)
	-.08493(94.9)	-.02600(91.5)	.99605(5.1)

TABLE # 13 (CONTINUED)   SUBJECT 11   SEGMENT PA AXES

DIRECTION COSINES (ANGLES) OF SEGMENT ANATOMICAL AXES
WITH RESPECT TO SEGMENT PA AXES
(RA) = [DAG] [DGP] (RP)

SEGMENTS			
R CALF	.71736(44.2)	-.69592(134.1)	.03298(88.1)
	.69644(45.9)	.71759(44.1)	-.00648(90.4)
	-.01915(91.1)	.02762(88.4)	.99944(1.9)
R FOOT	.98795(8.9)	.06745(86.1)	.13931(82.0)
	-.01843(91.1)	.94491(19.1)	-.32680(109.1)
	-.15368(98.8)	.32030(71.3)	.93477(20.8)
L FLAP	.94200(19.6)	-.31616(108.4)	-.11196(96.4)
	.26845(74.4)	.91089(24.4)	-.31340(108.3)
	.20107(78.4)	.26519(74.6)	.94300(19.4)
L THI-F	.96511(15.2)	-.24973(104.5)	.07872(85.5)
	.25343(75.3)	.96640(14.9)	-.04103(92.4)
	-.06583(93.8)	.05955(86.6)	.99605(5.1)
L CALF	.81850(35.1)	.57267(55.1)	.04593(87.4)
	-.57352(125.0)	.81916(35.0)	.00695(89.6)
	-.03364(91.9)	-.03203(91.8)	.99892(2.7)
L FOOT	.98768(9.0)	-.06350(93.6)	.14305(81.8)
	.01743(89.0)	.95293(17.6)	.30267(72.4)
	-.15553(98.9)	-.29645(107.2)	.94230(19.6)
R FARM+H	.98378(10.3)	.17236(80.1)	.04974(87.1)
	-.17802(100.3)	.97220(13.5)	.15209(81.3)
	-.02214(91.3)	-.15840(99.1)	.98711(9.2)
L FARM+H	.98592(9.6)	-.15543(98.9)	.06165(86.5)
	.16284(80.6)	.97626(12.5)	-.14286(98.2)
	-.03799(92.2)	.15089(81.3)	.98782(9.0)
R THIGH	.99226(7.1)	.12012(83.1)	-.03165(91.8)
	-.11885(96.8)	.99213(7.2)	.03941(87.7)
	.03613(87.9)	-.03534(92.0)	.99872(2.9)
L THIGH	.96759(14.6)	-.24685(104.3)	-.05331(93.1)
	.24374(75.9)	.96807(14.5)	-.05865(93.4)
	.06609(86.2)	.04376(87.5)	.99685(4.5)
TORSO	.98443(10.1)	.00220(89.9)	.17576(79.9)
	-.00106(90.1)	.99997(.4)	-.00706(90.4)
	-.17577(100.1)	.00676(89.6)	.98441(10.1)

TOTAL BODY

TOT BODY	.96615(15.0)	-.03805(92.2)	.25516(75.2)
	.04382(87.5)	.99892(2.7)	-.01621(90.9)
	-.25426(104.7)	.02679(88.5)	.96676(14.8)

TABLE # 14 SUBJECT 11 GLOBAL AXES

SEGMENT INERTIAL TENSOR AT SEGMENT CENTER OF GRAVITY
WITH RESPECT TO GLOBAL AXES

SEGMENTS			
HEAD	173580.	-5862.	26133.
	-5062.	210855.	3142.
	26133.	3142.	162892.
NECK	13692.	-303.	2233.
	-303.	15497.	220.
	2233.	220.	15720.
THORAX	3266945.	16077.	253768.
	16877.	2720380.	-16413.
	253768.	-16413.	2196974.
ABDOMEN	41754.	-19.	12.
	-19.	23441.	-18.
	12.	-18.	64332.
PELVIS	1085989.	-14386.	-62550.
	-14386.	745328.	5788.
	-62550.	5788.	1257085.
RU ARM	121995.	1770.	12995.
	1770.	126907.	-11884.
	12995.	-11884.	25160.
RF ARM	40259.	317.	1808.
	317.	38633.	-15895.
	1808.	-15895.	16968.
R HAND	11653.	434.	830.
	434.	8591.	-2765.
	830.	-2765.	4330.
LU ARM	108563.	-2589.	10670.
	-2589.	112176.	11625.
	10670.	11625.	24977.
LF ARM	56293.	875.	25.
	875.	45996.	17911.
	25.	17911.	17977.
L HAND	10824.	-29.	176.
	-29.	8273.	2236.
	176.	2236.	3588.
R FLAP	173394.	8873.	-467.
	8873.	230719.	15369.
	-467.	15369.	290916.
R THI-F	584221.	3851.	-51820.
	3851.	610822.	17367.
	-51820.	17367.	263753.

TABLE # 14 (CONTINUED)   SUBJECT 11   GLOBAL AXES

SEGMENT INERTIAL TENSOR AT SEGMENT CENTER OF GRAVITY
WITH RESPECT TO GLOBAL AXES

SEGMENTS			
R CALF	487912.	-3080.	-29141.
	-3080.	491522.	-29644.
	-29141.	-29644.	70744.
R FOOT	7019.	1208.	3346.
	1208.	30185.	-574.
	3346.	-574.	30275.
L FLAP	140492.	-11953.	-1611.
	-11953.	195294.	-13159.
	-1611.	-13159.	240568.
L THI-F	580497.	-5013.	-72923
	-5013.	605825.	-12719.
	-72923.	-12719.	266491.
L CALF	480239.	1181.	-8933.
	1181.	480806.	40974.
	-8933.	40974.	69393.
L FOOT	7335.	-1154.	3266.
	-1154.	31757.	511.
	3266.	511.	31931.
R FARM+H	188199.	6871.	13687.
	6871.	146633.	-73038.
	13687.	-73038.	52664.
L FARM+H	204768.	-1815.	5514.
	-1815.	164589.	75251.
	5514.	75251.	49489.
R THIGH	1662597.	11018.	-40072.
	11018.	1745789.	41139.
	-40072.	41139.	554891.
L THIGH	1572850.	-17010.	-90175.
	-17010.	1645263.	-20236.
	-90175.	-20236.	515355.
TORSO	10649335.	3918.	314429.
	3918.	9747021.	-91119.
	314429.	-91119.	3523789.

TOTAL BODY

TOT BODY	115201278.	311622.	-3039217.
	311622.	107625025.	-532665.
	-3039217.	-532665.	12657055.

TABLE # 15 SUBJECT 11 GLOBAL AXES

PERCENT OF VOLUME FROM FLOOR TO SPECIFIED HEIGHTS

HEIGHT	% HEIGHT	% VOLUME
172.95	100	100.00
169.49	98	99.60
166.03	96	98.65
162.57	94	97.30
159.11	92	96.10
155.65	90	95.34
152.19	88	94.22
148.73	86	93.83
145.27	84	93.29
141.81	82	92.12
138.36	80	90.01
134.90	78	87.98
131.44	76	84.33
127.98	74	80.19
124.52	72	75.83
121.06	70	71.69
117.60	68	69.29
114.14	66	65.24
110.68	64	63.40
107.23	62	60.75
103.77	60	56.27
100.31	58	52.70
96.85	56	50.09
93.39	54	46.03
89.93	52	41.83
86.47	50	37.56
83.01	48	33.31
79.55	46	30.63
76.10	44	26.37
72.64	42	24.41
69.18	40	21.78
65.72	38	20.19
62.26	36	17.41
58.80	34	16.19
55.34	32	14.58
51.88	30	13.13
48.42	28	11.82
44.97	26	10.68
41.51	24	9.97
38.05	22	8.85
34.59	20	7.65
31.13	18	6.44
27.67	16	5.69
24.21	14	4.43
20.75	12	3.94
17.29	10	3.35
13.84	8	2.96
10.38	6	2.49
6.92	4	2.19
3.46	2	1.52
0.00	0	-.00

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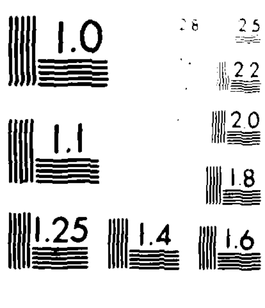

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